

STIC-Biotech/ChemLib

121108

From: Chan, Christina
Sent: Tuesday, May 04, 2004 1:22 PM
To: Wilder, Cynthia; STIC-Biotech/ChemLib
Subject: RE: Rush sequence search for 09/646,569

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Wilder, Cynthia
Sent: Tuesday, May 04, 2004 11:19 AM
To: Chan, Christina
Subject: Rush sequence search for 09/646,569

Ms. Chan,

I am requesting a rush sequence search for 09/646569 because this case needs prompt attention. Please forward your approval to STIC.

Please provide a standard search and for interference of SEQ ID NO: 60.

Thank you

Cynthia B. Wilder, Ph.D.
United States Patent and TradeMark Office
Carlisle Remson 2A35
Mailbox: 2C18
571/272-0791

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: 1
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 13:51:38 ; Search time 5401 Seconds

(without alignments)
11561.159 Million cell updates/sec

Title: us-09-646-569a-60

Perfect score: 2091

Sequence: 1 aagagacagacttaactc.....gagagagagggggggaagc 2091

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estcm:*
4: em_estcu:*
5: em_estov:*
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7: em_estro:*
8: em_hlc:*
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15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1919.8	91.8	2043	11	AF172821 Homo sapi
2	1909.4	91.3	2317	11	AF173551 Homo sapi
3	1889.6	90.4	1908	11	AF176919 Homo sapi
4	1878.6	89.8	1909	11	AF113212 Homo sapi

5	927	44.3	1019	13	EX354115
6	887.2	42.4	1201	9	AL523087
7	864.4	41.3	893	13	BQ940216
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10	801	38.3	921	13	BQ881763
11	796	38.1	880	12	B1752648
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13	775.4	37.1	841	13	BQ720852
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ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens MSTP092 (MST092) mRNA, complete cds.
DEFINITION AF172821
ACCESSION AF172821
VERSION AF172821.1 GI:33337985
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Liu, B., Song, L., Sheng, H., Qin, B.M., Liu, Y.Q., Zhao, B., Wang, X.Y., Zhang, Q., Ji, X.Y., Liu, B.H., Lu, H., Xu, H.S., Chen, J.Z., Cai, M.Q., Zheng, W.Y., Teng, C.Y., Liu, Q., Yu, L.T., Lin, J., Gong, J., Zhang, A.M., Gao, R.L. and Hu, R.T.
TITLE Submitted (28-JUL-1999) Molecular Medicine Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China
JOURNAL Location/Qualifiers
FEATURES
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Db	2041	AAA 2043	
RESULT 2	AF173551	2317 bp	linear
LOCUS	AF173551		HTC 01-AUG-2003
DEFINITION	Homo sapiens MSTP106 mRNA, complete cds.		
ACCESSION	AF173551		
VERSION	AF173551.1	GI:3337993	
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2317)		
AUTHORS	Liu,Y.Q., Sheng,H., Qin,B.M., Liu,B., Zhao,B., Wang,X.Y., Hu,J.R.T., Zhang,Q., Song,L., Liu,B.H., Lu,H., Xu,H.S., Zheng,W.Y. and Gong,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-JUL-1999) Molecular Medicine Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, Bei Li Shi Lu, Beijing, 100037, P.R. China		
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ORIGIN			
Query Match	91.3%; Score 1909.4; DB 11; Length 2317;		
Best Local Similarity	98.2%; Pred. No. 5.3e-303;		
Matches 2021; Conservative	0; Mismatches 11; Indels 25; Gaps 8;		
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Db	329	AAGCAGTGTGATAGCCTTCAAGCATGGAATATCTCCATCTCCCGCACAACATAC	388
QY	112	-----CGCTTTTGTTCCTTCACGTAAGACCTTTTAAATGCAATCTAACTAGG	164
Db	389	ACACACACACTTTTGTTCCTTCACGTAAGACCTTTTAAATGCAATCTAACTAGG	448
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Db	509	TACTCTCCATACCCCGTACTCAAAATTTCTACTGTATGAATTATGCTTAAATGAT	568
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Db	569	TCAGTGCAGAGAACTGTGAAATAAATATTTAATTTTTTTTATCCTTTACAA	628
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LOCUS AF113212 1909 bp mRNA linear HTC 12-APR-2002
 DEFINITION Homo sapiens MSTP032 mRNA, complete cds.
 ACCESSION AF113212
 VERSION AF113212.1 GI:11640571
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1909)
 AUTHORS Liu, B., Liu, Y. Q., Wang, X. Y., Zhao, B., Sheng, H., Zhao, X. W., Liu, S.,
 Xu, Y. Y., Ye, J., Song, L., Gao, Y., Zhang, C. L., Zhang, J., Wei, Y. J.,
 Qiang, H. Q., Zhao, Y., Liu, L. S., Ding, J. F., Gao, R. L., Wu, Q. Y.,
 Qiang, B. Q., Yuan, J. G., Liew, C. C., Zhao, M. S. and Hui, R. T.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
 Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
 Beijing 100037, P. R. China
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Db	1381	CCCTGGCCCTGTTCCTCCCTTCTCTCTCTCTCTCTCTTGCAAGAGAAATTTTAAATATTT	1440
QY	1573	GGGTCCACCTTCATATATATGTAATTAATTAATACATTTAAAGCATTTAAGCTCTCTTGA	1632
Db	1441	GGGTCCACCTTCATATATGTAATTAATTAATTAATTAAGCATTTAAGCTCTCTTGA	1500
QY	1633	AAATATCAACGGTTAAGGATAGCAAAACAAGAGAAATGCTGGAATTTGGCATCTGG	1692
Db	1501	AAATATCAACGGTTAAGGATAGCAAAACAAGAGAAATGCTGGAATTTGGCATCTGG	1560
QY	1693	AGACAGAGCAATCGAATTAATATTTGGCAAAAGTTCTTTTATGTGATATAGTGCAGGA	1752
Db	1561	AGACAGAGCAATCGAATTAATATTTGGCAAAAGTTCTTTTATGTGATATAGTGCAGGA	1620
QY	1753	TTTGAAGAGACTATTTTTTTTAAATGTGCACTAGCAACTCATCTTGGAAGACAGAGC	1812

Db	1621	TTTGAAGAGAGCTA-TTTTTTTTAAATGTTCCAACTGCAACTGACCTCATCTCTGGAAAGACACAGC	1679
Qy	1813	CAGAGAAATTAAGTAGAGGAAAGGTTATATAATCATTTGAGGACATTATGCCATAT	1872
Db	1680	CAGAGAAATCAAGTAGAGGAAAGGTTATATAATCATTTGAGGACATTATGCCATAT	1739
Qy	1873	ATTTTAATTCAGAAAAAATGTGTATTATCTTTAGATTGTTATTCATTCTTATGTA	1932
Db	1740	ATTTTAATTCAGAAAAAATGTGTATTATCTTTAGATTGTTATTCATTCTTATGTA	1799
Qy	1933	CTATGCACTCAGCTTCGTGGATTAATAAGACCAAAATATGATCTGTAACACATCA	1992
Db	1800	CTATGCACTCAGCTTCGTGGATTAATAAGACCAAAATATGATCTGTAACACATCA	1859
Qy	1993	CACATATTATTTAATATATATATCTATATACAGCCAAAAAATAAAAA	2041
Db	1860	CACATATTATTTAATATATATATCTATATACAAAAAATAAAAA	1908
RESULT 5			
LOCUS	BX354115	1019 bp	mRNA
DEFINITION	BX354115 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens		EST 05-MAY-2003
ACCESSION	BX354115		
VERSION	BX354115.1	GI:30371832	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1019)		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 379.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgl-bin/cluster.cgi?seq=CS0DC015AB06QPicluster=379.r. Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/InvitrogenCorporation 1600 Paradey Avenue Genoscope sequence ID : CS0DC015AB06QPI.		
FEATURES			
source	Location/Qualifiers		
	1..1019		
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	/clone="CS0DC015Y111"		
	/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"		
	/clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a Noci-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
ORIGIN			
Query Match	44.3%	Score 927;	DB 13; Length 1019;
Best Local Similarity	97.4%	Pred. No. 3.7e-142;	
Matches 930; Conservative	10; Mismatches 15;	Indels 0; Gaps 0;	
Db	1099	GTATCGAACACTTGCTTGGCAAGAGCTCTTAGTTAACAAATTTAGCAGCTACTGTTGT	1158
Qy	65	GGATGGAACACTTGCTTGGCAAGAGCTCTTAGTTAACAAATTTAGCAGCTACTGTTGT	124
Db	1159	GTTAAACACACTTTTACCAAAATAGTTCAGGCAAGCAGAGCAATGACTATTATTAAG	1218
Qy	125	GTTAAACACACTTTTACCAAAATAGTTCAGGCAAGCAGAGCAATGACTATTATTAAG	184

QY 1219 AAAGGCTTCCGAGCATCACTTAACATCCCAAACTAAAAAGATCAACTCTTCCAACTG 1278
 Db 185 AAAAGGCTTCCGAGCATCACTTAACATCCCAAACTAAAAAGATCAACTCTTCCAACTG 244
 QY 1279 AGAAAAGACTCCTGGCTTTGAATGAAAGCTTACAGCAGAGAGTCAACGCGCAACA 1338
 Db 245 AGAAAAGACTCCTGGCTTTGAATGAAAGCTTACAGCAGAGAGTCAACGCGCAACA 304
 QY 1339 ACAAAGCAACAACAACATTTGGATTTATTTCACTCACTGTTTAAATATACATCT 1398
 Db 305 ACAAGCAACAACAACAACATTTGGATTTATTTCACTCACTGTTTAAATATACATCT 364
 QY 1399 TATATATTTTCTAGTAGAGAAAGTCAAAATCAGCCTCTTCAACATTTATATACAGTTTAA 1458
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 QY 1459 TAAAGCTTCTGCAAGTCACTTGTCTCTCAGCCTGAGGATTTTCTCCCGCAGCTTGC 1518
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 QY 1579 AACTTCAAT 1638
 Db 545 AACTTCAAT 604
 QY 1639 CACAGGCTAAGGCAATGACAAAGCAAGAGAAATCTGAGAAATTTGGCACTGAGACAA 1698
 Db 605 CACAGGCTAAGGCAATGACAAAGCAAGAGAAATCTGAGAAATTTGGCACTGAGACAA 664
 QY 1699 GCAATCTGAAAT 1758
 Db 665 GCAATCTGAAAT 724
 QY 1759 GAGAGTATTTTCTTAT 1818
 Db 725 GAGAGTATTTTCTTAT 784
 QY 1819 AATGAGTAGAAGTGAAGAGTTTATATATATATATATATATATATATATATATAT 1878
 Db 785 AATGAGTAGAAGTGAAGAGTTTATATATATATATATATATATATATATATATAT 844
 QY 1879 AATTCAGAAAAT 1938
 Db 845 AATTCAGAAAAT 904
 QY 1939 GACTCATGCTTCTGATTAATATATATATATATATATATATATATATATATATAT 1998
 Db 905 GACTCATGCTTCTGATTAATATATATATATATATATATATATATATATATATAT 964
 QY 1999 TAT 2053
 Db 965 TAT 1019

RESULT 6
 AL523087 1201 bp mRNA linear EST 22-MAY-2003
 LOCUS AL523087 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DC001YH21 5-PRIME, mRNA sequence.
 ACCESSION AL523087
 VERSION AL523087.2 GI:31041348
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12786580.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 EMAIL: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 379.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC001YH21&cluster=379.r. Contact :
 Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DC001YH21.

FEATURES
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 1..1201
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC001YH21"
 /rname="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 42.4%; Score 897.2; DB 9; Length 1201;
 Best local similarity 97.7%; Pred. No. 1,1e-135;
 Matches 895; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1132 GTTAAAGTATTTAGACCTAATGTTTGTGTTAAACACACTTTTCAACCAATAGGTTCTGAG 1191
 Db 61 GATTAAGTATTTAGACCTAATGTTTGTGTTAAACACACTTTTCAACCAATAGGTTCTGAG 120
 QY 1192 GCAAGAGAGCAATGATTTTAAAGAAAGCTTTCCAGCATCACTTACATCCCA 1251
 Db 121 GCAAGAGAGCAATGATTTTAAAGAAAGCTTTCCAGCATCACTTACATCCCA 180
 QY 1252 AACTTAAAGATGATCTTCCAGCAAGAAAGATCCGAGTTTGAATGAAAGTTAC 1311
 Db 181 AACTTAAAGATGATCTTCCAGCAAGAAAGATCTCGGCTTGAATGAAAGTTAC 240
 QY 1312 AGCAGAGAGTCAAGGCAAGGCAACCAACCAACCAACCAATTTGAATATATTT 1371
 Db 241 AGCAGAGAGTCAAGGCAAGGCAACCAACCAACCAACCAATTTGAATATATTT 300
 QY 1372 CTCACTCAGGTTTAAAT 1431
 Db 301 CTCACTCAGGTTTAAAT 360
 QY 1432 CTTCTCAACATTTAT 1491
 Db 361 CTTCTCAACATTTAT 420
 QY 1492 GAGGATTTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
 Db 421 GAGGATTTTCTTCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 1552 GAGGAAATATTTAAATATTTGGTCCAACTTCAATATATATATATATATATATATAT 1611
 Db 481 GAGGAAATATTTAAATATTTGGTCCAACTTCAATATATATATATATATATATATAT 540
 QY 1612 GCATTTAATCTTCTTCTAGAAAATATGACAGGCTTAAAGGATGACAAAACAAAGGAA 1671
 Db 541 GCATTTAATCTTCTTCTAGAAAATATGACAGGCTTAAAGGATGACAAAACAAAGGAA 600
 QY 1672 TGCTGAGAAATTTGGCACTGAGAGCAAGCAATCTGAATATATATTTTCCAAAAGTTCTTT 1731
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 QY 1732 TTATGATATATAGTCAAGATTTGAAGAGCAATTTTATATATTTTGAATGCAACTAGCA 1791

[illegible]

OY		763	GCTTGTTGTAAGCTGAGTCTTGTGCATCCTCCATATTGGACGAAGAATATTTCTGACTTG	822
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OY		823	CAATGACGCTAAGTGTAAAAATTTATTTATTCATCCTAGAAAGCCTTGACTAGAAAATG	882
Dd		121	CAATGACGCTAAGTGTAAAAATTTATTTATTCATCCTAGAAAGCCTTGACTAGAAAATG	180
OY		883	AATAAATATTGAGGCTTTCCTGCCCATCTGGCTTGCACTGCGCAGAAGCAGAGATA	942
Dd		181	AATAAATATTGAGGCTTTCCTGCCCATCTGGCTTGCACTGCGCAGAAGCAGAGATA	240
OY		943	GAAATGTAAATCTTCACAACATCCAACAGATCCGAAACCAGGGGGTAGGCAATTCTATGTAGG	1002
Dd		241	GAAATGTAAATCTTCACAACATCCAACAGATCCGAAACCAGGGGGTAGGCAATTCTATGTAGG	300
OY		1003	TTTTGGACATGAAAGTTTGTGTGCATCTTGTTTATGCTGGCTCAACCTGCTATTAACCTCT	1062
Dd		301	TTTTGGACATGAAAGTTTGTGTGCATCTTGTTTATGCTGGCTCAACCTGCTATTAACCTCT	360
OY		1063	CTGGCTTAATAGTCTCTCATCTTATTAGACAAGACGTAATCGAACACTTGCTTGACCAA	1122
Dd		361	CTGGCTTAATAGTCTCTCATCTTATTAGACAAGACGTAATCGAACACTTGCTTGACCAA	420
OY		1123	GCGCTTTAGTTAAACAATTTAGACGTAAGTGTGTGTATTAACAACACTTTTCACCCAATA	1182
Dd		421	GCGCTTTAGTTAAACAATTTAGACGTAAGTGTGTGTATTAACAACACTTTTCACCCAATA	480
OY		1183	GCTTCTAGGCAACGAGAGCAATGACTATTTAAAGAAAGGCTTTCACAGATCACTTAC	1242
Dd		481	GCTTCTAGGCAACGAGAGCAATGACTATTTAAAGAAAGGCTTTCACAGATCACTTAC	540
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Dd		541	ACATCCGAAAACCTAAAAAGATCAACTCTTCCAACTGAGAAAAGACTCTGCGCTTTGTAATG	600
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OY		1363	AATATTAATTCGCACTCACGTTTAAATATACATCTTATTTATTTTCTAGTAGAAACT	1422
Dd		661	AATATTAATTCGCACTCACGTTTAAATATACATCTTATTTATTTTCTAGTAGAAACT	720
OY		1423	ACAAATCAGCCTCTTCAACAATTATTAATACGTTTAATAAAGCCTTGCAGTACTTGT	1482
Dd		721	ACAAATCAGCCTCTTCAACAATTATTAATACGTTTAATAAAGCCTTGCAGTACTTGT	780
OY		1483	CTTCAACCTGAGTATTTTCTGCCCAACCTTGCCCTGTCTCCCTCTCTCTCTC	1542
Dd		781	CTTCAACCTGAGTATTTTCTGCCCAACCTTGCCCTGTCTCCCTCTCTCTCTC	840
OY		1543	CCTTTGCAAGAGAAATATTTACATAATTT--GGGTCCAACTTCAATATATG	1591
Dd		841	CCTTTGCAAGAGAAATATTTACATAATTTGGGTCCAAACTTCAATATATG	891
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LOCUS BX354114 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens				
DEFINITION cDNA clone GS0D0015111 3-PRIME, mRNA sequence.				
ACCESSION BX354114				
VERSION BX354114.1 GI:30369794				
KEYWORDS EST.				
SOURCE Homo sapiens (human)				
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE 1 (bases 1 to 1047)				
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE Full-length cDNA libraries and normalization				
JOURNAL Unpublished (2001)				

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 379.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cgi?seq=CS0DC015AE06NP1&cluster=379.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0DC015AE06NP1.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/note="T1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 40.1%; Score 838; DB 13; Length 1047;
Best Local Similarity 94.4%; Pred. No. 1.3e-127;
Matches 847; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

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987 TCGACAGAGCTCTTACTGATTAACATTTAGACAGCTACTGTTGTGTTAAACACACTTTTC 838
1175 ACCAATGTTGTTGAGGCAACGAGAGCAATGACTATTAAAGAAAGGCTTTCCACGA 1234
837 ACCAATGTTGTTGAGGCAACGAGAGCAATGACTATTAAAGAAAGGCTTTCCACGA 778
1235 TCACCTACAGATCCCAAAATTAAGATCACTCTTCACTGAGAAAGAGCTCCGGC 1294
777 TAACCTACAGATCCCAAAATTAAGATCACTCTTCACTGAGAAAGAGCTCCGGC 718
1295 TTTGATGAAACTTACAGAGAGTCAAGGCCACGGCAACAACGACAAACA 1354
717 TTTGATGAAACTTACAGAGAGTCAAGGCCACGGCAACAACGACAAACA 658
1355 ACATTGGAATATATTTCTGACCTCAGCTTTAATATATCTTATATTTTCTGTA 1414
657 ACATTGGAATATATTTCTGACCTCAGCTTTAATATATCTTATATTTTCTGTA 598
1415 GAGAAACTACAAATCAGGCTCTTCAACATTTATATACAGTTTAAAGCCCTTGCAGT 1474
597 GAGAAACTACAAATCAGGCTCTTCAACATTTATATACAGTTTAAAGCCCTTGCAGT 538
1475 TACTTGTCTCTACCTCAGGATTTTCTTCTCCACCTTGCCTTCTCCCTCC 1534
537 CACTGTCTCTACCTCAGGATTTTCTTCTCCCTTGCCTTCTCCCTCCCTCC 478
1535 CTCTTCTCTCTTGAAGAGAAATATTTAATATTTGGTCCCACTTCAATATGTA 1594
477 CTCTTCTCTCTTGAAGAGAAATATTTAATATTTGGTCCCACTTCAATATGTA 418
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417 TAATTAATACATTAAGACATTTAATCTCTTCTTGAAGAAATGACAGGTTAGGATA 358
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1715 TTGGCAAAAGTTCTTTTATGTCATATAGTTCAGAGTTTGAAGAGACTATTTTCTTT 1774
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QY

1775 AATGTGCACTAGCACTCATCTTGGGAAACACAGCCAGAGAAATGAAGATGA 1834

Db

237 AATGTGCACTAGCACTCATCTTGGGAAACACAGCCAGAGAAATGAAGATGA 178

QY

1835 AAGCTTAAATCCATTTGTAGACATTTATCCCATATTTTAAATTAAGAAATG 1894

Db

177 AAGCTTAAATCCATTTGTAGACATTTATCCCATATTTTAAATTAAGAAATG 118

QY

1895 TGTTTATCTTGAATTTGTATTCATATCTTATGATGATGATGATGATGATG 1954

Db

117 TGTTTATCTTGAATTTGTATTCATATCTTATGATGATGATGATGATGATG 58

QY

1955 TAATTAAGACCAAA-ATATGATCTGTATACCAACATCAACATATATTAATA 2010

Db

57 TAATTAAGACCAAAATATGATCTGTATACCAACATTAATTAATA 1

RESULT 9

BUI51512 956 bp mRNA linear EST 03-SHP-2002

LOCUS

AGENCOURT_7982170 lupski_dorsal_root_ganglion Homo sapiens cDNA

DEFINITION

clone IMAGE:6186460 5', mRNA sequence.

ACCESSION

BUI51512.1 GI:2265044

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 956)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

FEATURES

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FEATURES

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FEATURES

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FEATURES

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FEATURES

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FEATURES

/tissue_type="dorsal root ganglia"

FEATURES

/dev_stage="adult, 36 yr"

FEATURES

/lab_host="DH10B"

FEATURES

/clone_lib="lupski_dorsal_root_ganglion"

FEATURES

/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACGTGTTCTAGTCGCGAGCGGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 39.8%; Score 831.6; DB 13; Length 956;
Best Local Similarity 96.5%; Pred. No. 1.5e-126;
Matches 888; Conservative 0; Mismatches 14; Indels 18; Gaps 3;


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QY 61 AAGCAGTGTAGTACGCTTCAGACGTGTAATATCTCCATCTTCCGCGC----- 111
DB 96 AAGCAGTGTAGTACGCTTCAGACGTGTAATATCTCCATCTTCCGCGCACACATAC 155
QY 112 -----CGCTTTTGTTCCTTTCAGTAGACACCTTTTAAATGACAGACTTAAC 164
DB 156 ACACACACACTTTTGTTCCTTTCAGTAGACACCTTTTAAATGACAGACTTAAC 215
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QY 345 AGCAGTGAATTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 404
DB 396 AGCAGTGAATTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 455
QY 405 GCTGTTAATTTATTTTCCAAAGAGTAATAGACATGCAAAAGTTCAATTAATACTG 464
DB 456 GCTGTTAATTTATTTTCCAAAGAGTAATAGACATGCAAAAGTTCAATTAATACTG 515
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DB 636 AATATTGAACCTGCTCCCTGAGCAGGCAATTTCCCTTTCCGAGAGTTTACAGT 695
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QY 825 ATGCAGCTAGAT- GTAAAAATTTTATTCATCTAG- AAGCCTTGATGAGAAAATG 882
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QY 883 AATAAATATGAGAGTTTCG 902
DB 936 AATAAATATGAGAGTTTCG 955

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RESULT 10
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LOCUS BO881763
DEFINITION AGENCOURT 7978342 lupski dorsal root ganglion Homo sapiens cDNA
ACCESSION BO881763
VERSION BO881763.1 GI:22273771
KEYWORDS EST.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgi.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13575 row: 9 column: 11
High quality sequence stop: 670.
Location/Qualifiers
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/clone="IMAGE:6185122"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/notes="Vector: pCMV-SPORT (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCACGCGTCG-3' and
5'-GCTAGTCTGATGAGCGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

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ORIGIN

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Query Match 38.3%; Score 801; DB 13; Length 921;
Best Local Similarity 98.8%; Pred. No. 1.6e-121;
Matches 848; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
112 CGCTTTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTTCA 171
DB CACTTTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTTCA 87
QY 172 GTAACTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTTCA 231
DB 88 GTAACTTGTTCCTTCAGGTAGACACCTTTTAAATGAGAACTAAGGCAATTTCA 147
QY 232 CATACCCGTAATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 291
DB 148 CATACCCGTAATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 207
QY 292 CAAGAGAACTGTGTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 351
DB 208 CAAGAGAACTGTGTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 267
QY 352 GATTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
DB 268 GATTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 327
QY 412 AATATTTTCCAAAGATATAGACATGCAAAAGTTTCATTAATAAATCTGGCCATTAA 471
DB 328 AATATTTTCCAAAGATATAGACATGCAAAAGTTTCATTAATAAATCTGGCCATTAA 387
QY 472 AATAATTAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
DB 388 AATAATTAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 447

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QY 532 ACAATTGAGATCGTTGAAAAAGCTAGTATATTTCAGAGAAATGATTTTATTATTG 591
 Db 448 ACAAAATTGAGATCGTTGAAAAAGCTAGTATATTTCAGAGAAATGATTTTATTATTG 507
 QY 592 AAACGTCTCCCTAGCAGGCGATTTCCCTTTTCTGCGAGATTAGCAAGTTTAGAG 651
 Db 508 AAACGTCTCCCTAGCAGGCGATTTCCCTTTTCTGCGAGATTAGCAAGTTTAGAG 567
 QY 652 AGAATGTGATGAAAAAGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 711
 Db 568 AGAATGTGATGAAAAAGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
 QY 712 CTCAGACCTATGACGTAATCCCTTCTGCTAGAAATATTATAGAGAGCTCAGCTGATG 771
 Db 628 CTCAGACCTATGACGTAATCCCTTCTGCTAGAAATATTATAGAGAGCTCAGCTGATG 687
 QY 772 AAACGTGTTTGTGATCTTCATCTTCATATTTGCAAGAAAGTATTTTCTGACTTGCAATGCA 831
 Db 688 AAACGTGTTTGTGATCTTCATCTTCATATTTGCAAGAAAGTATTTTCTGACTTGCAATGCA 747
 QY 832 TGAGTGTAAATTTATTTATATCATCTGTAAGAAAGCTGAGTAAATGAAATGAAAT 891
 Db 748 TGAGTGTAAATTTATTTATATCATCTGTAAGAAAGCTGAGTAAATGAAATGAAAT 806
 QY 892 TGAGGTTTCTGCTCATATCT-GGCTTGCAATGTGCG-AGAAAGCAGAGAAATGAAATG 949
 Db 807 TGAGGTTTCTGCTCATATCTGCGGCTTGCAATGTGCGAAAGCAGAGAAATGAAATG 866
 QY 950 TAA-TCTCCAACTCCAA 966
 Db 867 TAATCTCCAACTCCAA 884

RESULT 11
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 LOCUS 603021702F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192376 5',
 DEFINITION mRNA sequence.
 ACCESSION B1752648
 VERSION B1752648.1 GI:15744226
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 880)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNM at:
 http://image.llnl.gov
 Plate: LLNM11481 row: c column: 01
 High quality sequence stop: 795.
 Location/Qualifiers
 1. 880
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5192376"
 /lab_host="DH10B"
 /clone_1ib="NIH MGC 114"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains; age range 23-27 yo. library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed

ORIGIN

upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH-MGC Library."

Query Match 38.1%; Score 796; DB 12; Length 880;
 Best Local Similarity 98.0%; Pred. No. 1,1e-120;
 Matches 816; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1230 CAGCATCCTTACACATCCCAAACTTAAAGATCACTCTTCCAATGAGAAAGACTC 1289
 Db 1 CAGCATCCTTACACATCCCAAACTTAAAGATCACTCTTCCAATGAGAAAGACTC 60
 QY 1290 CTGGCTTTGATGAAAGCTTACAGCAGAGAGTCAAGGCGCAAGCAACAGCAAC 1349
 Db 61 CTGGCTTTGATGAAAGCTTACAGCAGAGAGTCAAGGCGCAAGCAACAGCAAC 120
 QY 1350 AACAACTTTGGAATTTATTTCTCAACCTGTTTATATATACATCTTATTTTTC 1409
 Db 121 AACAACTTTGGAATTTATTTCTCAACCTGTTTATATATACATCTTATTTTTC 180
 QY 1410 TAGTAGAGAACTPACAAATGAGCTCTTCAACATTTATATACAGTTTATAGCTCTTG 1469
 Db 181 TAGTAGAGAACTPACAAATGAGCTCTTCAACATTTATATACAGTTTATAGCTCTTG 240
 QY 1470 CAAGTTCTGTTCTGCTCAGCTGAGGATTTTCTGCTCCGCACTTGCCCTGTTCTG 1529
 Db 241 CAAGTTCTGTTCTGCTCAGCTGAGGATTTTCTGCTCCGCACTTGCCCTGTTCTG 300
 QY 1530 CCTTCCTCTTCTGCTTGGCAAGAGAAATATTTAAATTTGGTCCACTTCAATTA 1589
 Db 301 CCTTCCTCTTCTGCTTGGCAAGAGAAATATTTAAATTTGGTCCACTTCAATTA 360
 QY 1590 TGTAAATTTATATACATTTAAAGCACTTAACTTCTGCTTGGCAAGAGAGAGCTAG 1649
 Db 361 TGTAAATTTATATACATTTAAAGCACTTAACTTCTGCTTGGCAAGAGAGAGCTAG 420
 QY 1650 GCATAGACAAAGAGAGAAATGCTGAGAAATTTGCACTGAGACAGCAAGCAATCTGAAT 1709
 Db 421 GCATAGACAAAGAGAGAAATGCTGAGAAATTTGCACTGAGACAGCAAGCAATCTGAAT 480
 QY 1710 AAATATTTGGCAAAAGTCTTTTATATGCTATATAGTCAAGATTTGAGAGACTATTT 1769
 Db 481 AAATATTTGGCAAAAGTCTTTTATATGCTATATAGTCAAGATTTGAGAGACTA-TTT 539
 QY 1770 TTTTATGTTGCAACTAGCACTCATCTCGGAGACACAGCCAGAGAGATGATGATAG 1829
 Db 540 TTTTATGTTGCAACTAGCACTCATCTCGGAGACACAGCCAGAGAGATGATGATAG 599
 QY 1830 AGTGAAGGTTTATTAATTCATTTGTAAGCACTTATTCATATTTTAAATCAAGAA 1889
 Db 600 AGTGAAGGTTTATTAATTCATTTGTAAGCACTTATTCATATTTTAAATCAAGAA 659
 QY 1890 AATTGTTTATCTTATAGAAATTTGATTCATATCTTATATGATCTATGACTCATGCT 1949
 Db 660 AATTGTTTATCTTATAGAAATTTGATTCATATCTTATATGATCTATGACTCATGCT 719
 QY 1950 CTGGATTAATTAAGACCAAAATGTATCTGTATACCAATCACAATATTTATTTAAT 2009
 Db 720 CTGGATTAATTAAGACCAAAATGTATCTGTATACCAATCACAATATTTATTTAAT 779
 QY 2010 ATATATCTATATACAGCCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
 Db 780 ATATATCTATATACAGCTCCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832

RESULT 12
 AL523086/c 1168 bp mRNA linear EST 22-MAY-2003
 LOCUS AL523086 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS00C001YH21 3-PRIME, mRNA sequence.

ACCESSION AL523086.2 GI:31041347
 VERSION AL523086.2
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1168)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization.
 Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:12786579.
 COMMENT
 Contact: Genoscope - Centre National de Sequencage
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 379.r for more information about this cluster, see
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC001CD1INP1&cluster=379.r. Contact : Feng Liang Email : fliang@life.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC001CD1INP1.
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC001YH21"
 /issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_1b="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 37.5%; Score 783.4; DB 9; Length 1168;
 Best Local Similarity 91.8%; Pred. No. 1e-118;
 Matches 809; Conservative 11; Mismatches 61; Indels 0; Gaps 0;

QY 1132 GTTACATTTAGACGCTACTGTTGTGTTAAACACACTTTTACCAATAGCTTGAAG 1191
 DB 881 GATTAACATTTGGCGGCTACTGTTGTGTTAAACACACTTTTACCAATAGCTTGAAG 822
 QY 1192 GCAACGAGAGCAATGACTATTAAAGAAAGCTTCCAGATCATCTTACATCCCA 1251
 DB 821 GSAACGAGGGAATGACTATTAAAGAAAGCTTCCAGATCATCTTACATCCCA 762
 QY 1252 AACTAAAAAGTCACTCTTCCAACTGAGAAAAAGACTCTGCTTGAATGGAACCTTAC 1311
 DB 761 GACTAAAGAGTCACTCTTCCGACGAGARAGACTCTGCTTGAATGAGARACTCAC 702
 QY 1312 AGCAGAGGTCAGAGGCCACGCAACAACAAGCAACAACAACATTTGGAATTTTAT 1371
 DB 701 VGGARAGARTTAAGGCCACCGCACCAACAACAACAACAACAACAATTTTAT 642
 QY 1372 CTCACATCAAGTTTATATACATCTTATTTTCTAGTAGAGAACTACAATCAG 1431
 DB 641 CTCACATCAAGTTTATATACCTCTTATTTTCTAGTAGAGAACTACAATCAG 582
 QY 1432 CCTCTTCAACATTTATATACAGTTTAAAGCTCTTGAAGTACTTGTCTCAGCT 1491
 DB 581 CCTCTTCAACATTTATATACAGTTTAAAGCTCTTGAAGTACTTGTCTCAGCT 522
 QY 1492 GAGGATATTTTCTCCCACTTGCCTGCTCTCTCCCTCTCTCTCTCTCTCTCTGCA 1551
 DB 521 TAGGATATTTTCTCCCTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTGCA 462
 QY 1552 GAGGAAATTTTAACTATTTGGGTGCACTTAAATATATATATATATATATATAT 1611
 DB 461 GAGGAAATTTTAACTATTTGGGTGCACTTAAATATATATATATATATATATAT 402

QY 1612 GCATTTACTCTCTTCTGAAAAATGCAAGGCTAAGCATAGACAAACAAAGGAAA 1671
 DB 401 GCATTTACTCTCTCTTCTGAAAAATGCAAGGCTAAGCATAGACAAACAAAGGAAA 342
 QY 1672 TGCTGAGAAATTTGCACGAGGAGAGACAGCAATCTGAATTAATTTGCCAAAGTCTTT 1731
 DB 341 TGCTGAGAAATTTGCACGAGGAGAGACAGCAATCTGAATTAATTTGCCAAAGTCTTT 282
 QY 1732 TTATGTCATATAGTGTGAGATTTGAAGAGCTATTTTATATGTTGCAATGCA 1791
 DB 281 TTTTTCATATATAGTGTGAGATTTGAAGAGCTATTTTATATGTTGCCATGCA 222
 QY 1792 CTATCTTGGAGAGACAGCCGAGCATAGTAAAGTAAAGTTATATCCAT 1851
 DB 221 NTATCTTGGGAAAAACGCGAGGAATGAATGAAGTGAAGGTTATATCCAT 162
 QY 1852 TTGTAAACATTTTCCCATATTTTAAATTCAGAAAAATGTGTTATCTTTAGAAAT 1911
 DB 161 TTGTAAACATTTTCCCATATTTTAAATTCAGAAAAATGTGTTATCTTTAGAAAT 102
 QY 1912 TTGTATTCATATCTTTATGACTATGCTCATGCTTCTGATTAATAAGCAACCAAT 1971
 DB 101 TTGTATTCATATCTTTATGACTATGCTCATGCTTCTGATTAATAAGCAACCAAT 42
 QY 1972 ATGATCTGTACACATCAACATATATATATATATA 2012
 DB 41 ATGATCTGTACACATCAACATATATATATATATA 1

RESULT 13
 BQ720852 841 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOUR 8241231 lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6187117 5', mRNA sequence.
 ACCESSION BQ720852
 VERSION BQ720852.1 GI:21859749
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 841)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: gcaps-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM3580 row: 3 column: 14
 High quality sequence stop: 700.

FEATURES

source

1..841
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6187117"
 /sex="male"
 /issue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_1b="lupski_sympathetic_trunk"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site: 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCACCAACGCGTCCG-3' and 5'-GACTAGTTCATGATCCGAGGCGCCCT(15)-3'. Size selected >

ORIGIN

1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

Query Match 37.1%; Score 775.4; DB 13; Length 841; Best Local Similarity 97.2%; Pred. No. 2.5e-117; Matches 805; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

77 CTTCAAGCATGTAATAATCTTCATCTTCCCGCCG-----CTTTTGG 120
 1 CTTCAAGCATGTAATAATCTTCATCTTCCCGCCGACATACACACACACTTTTGG 60
 121 TTTCTTTAGGTAGACACCTTTTAAAGCAAACTACTAGGCACTTTCAGTACTTGG 180
 61 TTTCTTTAGGTAGACACCTTTTAAAGCAAACTACTAGGCACTTTCAGTACTTGG 120
 181 CTTTCAAAATCAATAAGTCAATGTAATGGAACATTTTGGCCCTACTCTCCATACCCG 240
 121 CTTTCAAAATCAATAAGTCAATGTAATGGAACATTTTGGCCCTACTCTCCATACCCG 180
 241 TGACTCAAAATCTCTACTGTAATGTAATGCTTTAAAGTAAATTCAGTCAAGGAA 300
 181 TGACTCAAAATCTCTACTGTAATGTAATGCTTTAAAGTAAATTCAGTCAAGGAA 240
 301 CTTGGTGAATAATAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 360
 241 CTTGGTGAATAATAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 300
 361 TGGTTGATGTGTGCTCTGTACACAAGCCATTTCATAGATGAGCTGTTAATTTTTC 420
 301 TGGTTGATGTGTGCTCTGTACACAAGCCATTTCATAGATGAGCTGTTAATTTTTC 360
 421 CAAAGAGTAATAGCATGCAAAAGTTTCAATAAATCGGCGCATTAACAATAATTA 480
 361 CAAAGAGTAATAGCATGCAAAAGTTTCAATAAATCGGCGCATTAACAATAATTA 420
 481 TAAACTAATAAGCATTCCTCTAGGTTTTTCCAACTGCTATCCATTAACAATAATTTG 540
 421 TAAACTAATAAGCATTCCTCTAGGTTTTTCCAACTGCTATCCATTAACAATAATTTG 480
 541 AGAATCGTTGAAAAAGCTAGTATATTTTCAAGAAAAAGATTTTCAATTAAGAACTGTTG 600
 481 AGAATCGTTGAAAAAGCTAGTATATTTTCAAGAAAAAGATTTTCAATTAAGAACTGTTG 540
 601 TCCCTAGAGGCAATTTTCCCTTTTCTGAGGATTAGCAAGTTTGAAGAGATAGTC 660
 541 TCCCTAGAGGCAATTTTCCCTTTTCTGAGGATTAGCAAGTTTGAAGAGATAGTC 600
 661 ATGAAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 720
 601 ATGAAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 660
 721 ATGAAAGCAATCCCTTGTCTAGAAATTTTAAAGGAGCTCAGTTGTTGAAGAGAGT 780
 661 ATGAAAGCAATCCCTTGTCTAGAAATTTTAAAGGAGCTCAGTTGTTGAAGAGAGT 720
 781 TTTGTCAATCTTCATATTTTGAAGAGGAAATTTTCTAGCTGCAATGCACTAGATGTA 840
 721 TTTGTCAATCTTCATATTTTGAAGAGGAAATTTTCTAGCTGCAATGCACTAGATGTA 780
 841 AATTTTATTTTATCATCTGAAAGGCTTGAAGGAAATTTTGAAGGAAATTTTGAAGGAA 888
 781 AATTTTATTTTATCATCTGAAAGGCTTGAAGGAAATTTTGAAGGAAATTTTGAAGGAA 828

RESULT 14

BUS68349 797 bp mRNA linear EST 16-SEP-2002
 BUS68349 AGNCOURT_1040538 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:661581
 DEFINITION 5', mRNA sequence.

ACCESSION BUS68349 GI:22518649
 VERSION BUS68349.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaab@remail.nih.gov
 Tissue Procurement: CLONTECH

CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at:
 http://image.llnl.gov
 Plate: LLCW2857 row: f column: 21
 High quality sequence stop: 566.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
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 /clone_1lib="NIH_MGC_82"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatcagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCAATTAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAAGCCGCGAGCGCGCAATGCGC-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 36.2%; Score 757.8; DB 13; Length 797; Best Local Similarity 96.3%; Pred. No. 2e-114; Matches 765; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

1273 CAATGAGAAAGACTCTCGGCTTGAATGAACTTACAGAGAGTCAAGGCCACG 1332
 3 CAATGAGAAAGACTCTCGGCTTGAATGAACTTACAGAGAGTCAAGGCCACG 62
 1333 GCAACACACGACACAAACAAATTTGGAATATTATTCTCACTCACTTTAATAT 1392
 63 GCAACACACGACACAAACAAATTTGGAATATTATTCTCACTCACTTTAATAT 122
 1393 ACATCTTATTTTCTTCTAGTAAAGAACTCAATCGCCTCTCAACATTTATACA 1452
 123 ACATCTTATTTTCTTCTAGTAAAGAACTCAATCGCCTCTCAACATTTATACA 182
 1453 GTTATATAAGCTCTGGAAGTACTTGTCTCTCACTGAGATATTTTCTCCCA 1512
 183 GTTATATAAGCTCTGGAAGTACTTGTCTCTCACTGAGATATTTTCTCCCA 242
 1513 CTTGCCCCCTGCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1572
 243 CTTGCCCCCTGCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
 1573 GGGTCAACTCAATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1632
 303 GGGTCAACTCAATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 362
 1633 AAAATGCAAGGCTTAAGCATTAAGCAAAAGAAAGAAAGTCTAGAAATTTGCCACTGG 1692
 363 AAAATGCAAGGCTTAAGCATTAAGCAAAAGAAAGAAAGTCTAGAAATTTGCCACTGG 422

QY 1693 AGACAGCAATCTGATAATAATTTGGCAAAAGTCTTTTATGTCATATAGTGCAGGA 1752
 DB 423 AGACAGCAATCTGATAATAATTTGGCAAAAGTCTTTTATGTCATATAGTGCAGGA 482
 QY 1753 TTTGAGAGAGCTATTTTTTTTAAATGTTGCAACTAGCAACTCATCTTGGAGAGACAGC 1812
 DB 483 TTTGAGAGAGCTATTTTTTTTAAATGTTGCAACTAGCAACTCATCTTGGAGAGACAGC 542
 QY 1813 CAGGAGATGAGTGAAGTGAAGCTTAAATCCATTTGTAGATTTATCCCAT 1872
 DB 543 CAGGAGATGAGTGAAGTGAAGCTTAAATCCATTTGTAGATTTATCCCAT 602
 QY 1873 ATTTAAATTCAGAAAAATGTTGTTATCTTTAGATTTGTATTCATCTTATGTA 1932
 DB 603 ATTTAAATTCAGAAAAATGTTGTTATCTTTAGATTTGTATTCATCTTATGTA 662
 QY 1933 CATGTGACTCATGCTTCTGATTAATAAGACCAATATGTCATCCACATCA 1992
 DB 663 CATGTGACTCATGCTTCTGATTAATAAGACCAATATGTCATCCACATCA 722
 QY 1993 CACATATATATTAATAATATATCTATATTAACAGCCAAAAAAGAGAGAGAA 2052
 DB 723 CACATATATATTAATAATATATCTATATTAACAGCCAAAAAAGAGAGAA 782
 QY 2053 AAAGAGAGAGAGG 2066
 DB 783 ANNNAAAAACATG 796
 RESULT 15
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 LOCUS 603022001P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192352 5',
 DEFINITION mRNA sequence.
 ACCESSION BI752817
 VERSION BI752817.1 GI:15744395
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 795)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 http://image.llnl.gov
 Plate: LLM11481 row: b column: 01
 High quality sequence step: 792.
 Location/Qualifiers
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 /clone="IMAGE:5192352"
 /lab_host="DH10B"
 /clone_1fb="NIH_MGC_114"
 /note="Torgan: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:

ORIGIN this is a NIH_MGC Library."
 Query Match 35.0%; Score 732.4; DB 12; Length 795;
 Best Local Similarity 98.7%; Pred. No. 2.8e-110;
 Matches 780; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
 QY 1230 CAGCATCACTTACACATCCCAAACTAAAGATCACTCTTCCACTGAGAGAAAGACTC 1289
 DB 1 CAGCATCACTTACACATCCCAAACTAAAGATCACTCTTCCACTGAGAGAAAGACTC 60
 QY 1290 CTGGCTTTGAATGGAACCTTACAGCAGAGAGTCAAGGCGGACGATTAACAACGACAC 1349
 DB 61 CTGGCTTTGAATGGAACCTTACAGCAGAGAGTCAAGGCGGACGATTAACAACGACAC 120
 QY 1350 AACCAACATTTGGAAATATATTTCTCACTCAGCTTTTAAATTAATACATCTTATTTTC 1409
 DB 121 AACCAACATTTGGAAATATATTTCTCACTCAGCTTTTAAATTAATACATCTTATTTTC 180
 QY 1410 TAGTAGAGAACTCAAAATCAGCTCTTCAATTTATACAGTTTAAAGCCTCTTG 1469
 DB 181 TAGTAGAGAACTCAAAATCAGCTCTTCAATTTATACAGTTTAAAGCCTCTTG 240
 QY 1470 CAAGTACTGTTCTCTGCACTGAGGATTTTTCCTCCGACCTGCGCTGCTCTC 1529
 DB 241 CAAGTACTGTTCTCTGCACTGAGGATTTTTCCTCCGACCTGCGCTGCTCTC 300
 QY 1530 CCTTCCTCTGCTCCCTTTCAGAGAGAAATTTTAAATTTGGGTCACATTA 1589
 DB 301 CCTTCCTCTGCTCCCTTTCAGAGAGAAATTTTAAATTTGGGTCACATTA 360
 QY 1590 TGTAAATTA-TTAAATATTAAGATTTAACTCTCTTCTGAAATAATGACAGGCTAA 1648
 DB 361 TGTAAATTAATTAATTAATTAAGATTTAACTCTCTTCTGAAATAATGACAGGCTAA 420
 QY 1649 GGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACACAGCAATCTGAA 1708
 DB 421 GGCATAGACAAAACAAAGAGAAATGCTGAGAAATTTGCCACTGAGACACAGCAATCTGAA 480
 QY 1709 TAAATTTTGGCCAAAGTCTTTTATGTCATATATGTCAGATTTGAGAGAGCTATTT 1768
 DB 481 TAAATTTTGGCCAAAGTCTTTTATGTCATATATGTCAGATTTGAGAGAGCTATTT 539
 QY 1769 TTTTAAATGTTGCACTGACCACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTAG 1828
 DB 540 TTTTAAATGTTGCACTGACCACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTAG 599
 QY 1829 AAGTGAAGGTTTAAATTCATCTTGTAAAGCATTTATCCCATATATTTTAAATTCAGAA 1888
 DB 600 AAGTGAAGGTTTAAATTCATCTTGTAAAGCATTTATCCCATATATTTTAAATTCAGAA 659
 QY 1889 AAATGAGTTTATCTTAAAGATTTTGTATTCAA-TACTTAAAGTACTATGTCATGCTATGC 1947
 DB 660 AAATGAGTTTATCTTAAAGATTTTGTATTCAAAGTACTTAAAGTACTATGTCATGCTATGC 718
 QY 1948 TTCTGATTAATTAAGACCAATATGATCTGTAACCAATCACAATCACAATATTAATTA 2007
 DB 719 TTCTGATTAATTAAGACCAATATGATCTGTAACCAATCACAATCACAATATTAATTA 778
 QY 2008 ATATATATCT 2017
 DB 779 ATATATATCT 788
 Search completed: May 5, 2004, 17:58:49
 Job time : 5411 secs

PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 3674
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-276-73

Query Match 95.8%; Score 2003.8; DB 13; Length 3674;
Beet Local Similarity 98.9%; Freq. No. 0;
Matches 2034; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

QY 1 AAGAGACAGACTATTAAGTCAAGTAAATTAAGAGAGATGTTCCATGTTATTTGTA 60
DB 1617 AAGAGACAGACTATTAAGTCAAGTAAATTAAGAGAGATGTTCCATGTTATTTGTA 1676
QY 61 AAGAGAGTGAATAGCTTCAAGATGTAATATCTTCAATCTTCCCGC----- 111
DB 1677 AAGAGAGTGAATAGCTTCAAGATGTAATATCTTCAATCTTCCCGC----- 111
QY 112 -----CGTTTGTGTTCTTCAAGTGAACCTTTTAAATGAGAACTAAGTGAAG 164
DB 1737 AACAACACACTTTTGTGTTCTTCAAGTGAACCTTTTAAATGAGAACTAAGTGAAG 1796
QY 165 CATTCACTAACTTTGCTTCAATCAATAAAGTCAATGATGAGAACTTTGTCGC 224
DB 1797 CATTCACTAACTTTGCTTCAATCAATAAAGTCAATGATGAGAACTTTGTCGC 1856
QY 225 TACCTCCATACCCCGGTACTCAATGCTACTGATGATTAAGTCTTAAGTGAAT 284
DB 1857 TACCTCCATACCCCGGTACTCAATGCTACTGATGATTAAGTCTTAAGTGAAT 1916
QY 285 TCACTGCCAAGAGAACTTGTGTAATTAATTTTATTTTATTTTATCCCTTACAA 344
DB 1917 TCACTGCCAAGAGAACTTGTGTAATTAATTTTATTTTATTTTATCCCTTACAA 1976
QY 345 AGCCATGATTTTATTTGTTGATGCTGCTGTAACAAGCATTTCAATGATGGA 404
DB 1977 AGCCATGATTTTATTTGTTGATGCTGCTGTAACAAGCATTTCAATGATGGA 2036
QY 405 GCTGTTATTTTCCCAAGATTAATGACATGCAAAAGTTCAATPAAACCTGGGCCA 464
DB 2037 GCTGTTATTTTCCCAAGATTAATGACATGCAAAAGTTCAATPAAACCTGGGCCA 2096
QY 465 TTAACAATAAATTAATTAAGCATTCCTCTAGGTTTTCGCAAACTGGCTTA 524
DB 2097 TTAACAATAAATTAATTAAGCATTCCTCTAGGTTTTCGCAAACTGGCTTA 2156
QY 525 TCCATAACAATTTGGAATCGTGAAGAAAGCTAGTATTAATTCAAGAAAGATTTTC 584
DB 2157 TCCATAACAATTTGGAATCGTGAAGAAAGCTAGTATTAATTCAAGAAAGATTTTC 2216
QY 585 ATTAATGAACCTGCTCCCTAGCAGGCAATTTCCCTTTTCTGGAGTTTACAGAGT 644
DB 2217 ATTAATGAACCTGCTCCCTAGCAGGCAATTTCCCTTTTCTGGAGTTTACAGAGT 2276
QY 645 TTAAGAGAGATTAATGATGAGAAAGAGAGAAAGAGAGAGAGAGAGAGATTAATA 704
DB 2277 TTAAGAGAGATTAATGATGAGAAAGAGAGAAAGAGAGAGAGAGAGAGATTAATA 2336
QY 705 GTAAGTCTCAGACCTATGAAGCTAATCCCTTGTCTAGAAATATTTAGAGAGCTCAGC 764
DB 2337 GTAAGTCTCAGACCTATGAAGCTAATCCCTTGTCTAGAAATATTTAGAGAGCTCAGC 2396
QY 765 TTGGTTGAACCTGAGTTTGTCACTTCATATTTTGACAGAGATTTTCTGACTTGA 824

DB 2397 TTGGTTGAACCTGAGTTTGTCACTTCATCTTCCATTTTGACAGAGATTTTCTGACTTGA 2456
QY 825 ATGCACTGATGATTAATTTTATTTTATCTTCAAGAAAGCTTGAAGAAATGAA 884
DB 2457 ATGCACTGATGATTAATTTTATTTTATCTTCAAGAAAGCTTGAAGAAATGAA 2516
QY 885 TAAATATGAGGTTTCCCTGATATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 944
DB 2517 TAAATATGAGGTTTCCCTGATATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2576
QY 945 AAATGATCTCCAACTCAAGATCGAAGCCAAAGGGTGAAGGATTTATGAGTT 1004
DB 2577 AAATGATCTCCAACTCAAGATCGAAGCCAAAGGGTGAAGGATTTATGAGTT 2636
QY 1005 TTGACATGAACTTTGATGATCTGATGATGATGATGATGATGATGATGATGATGAT 1064
DB 2637 TTGACATGAACTTTGATGATCTGATGATGATGATGATGATGATGATGATGATGAT 2696
QY 1065 GCTTATAGTCTTCAATCTATTAAGACAGCAGTATGAACTTGTGCAAGG 1124
DB 2697 GCTTATAGTCTTCAATCTATTAAGACAGCAGTATGAACTTGTGCAAGG 2756
QY 1125 CTCTTATGTTAACTTTAGAGCTACTGTTGTGTTAAACACTTTTACCAATAGG 1184
DB 2757 CTCTTATGTTAACTTTAGAGCTACTGTTGTGTTAAACACTTTTACCAATAGG 2816
QY 1185 TTCTGAGGCAACGAGAGATGATCTATTTAAGAAAGCTTTCCAGACATCACTTAAC 1244
DB 2817 TTCTGAGGCAACGAGAGATGATCTATTTAAGAAAGCTTTCCAGACATCACTTAAC 2876
QY 1245 ATCCCAAACTAAGAAATGATCTTCCAACTGAGAAAGCTCTGCTTGAATGGA 1304
DB 2877 ATCCCAAACTAAGAAATGATCTTCCAACTGAGAAAGCTCTGCTTGAATGGA 2936
QY 1305 AACTTACAGAGAGATGATCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1364
DB 2937 AACTTACAGAGAGATGATCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2996
QY 1365 TATTAATCTCAACCTGTTTAAATTAATCAATCTTATTTTCTAGTGAAGAACTAC 1424
DB 2997 TATTAATCTCAACCTGTTTAAATTAATCAATCTTATTTTCTAGTGAAGAACTAC 3056
QY 1425 AATCAAGCTCTCAACCTTATTAATCAAGTAAATCAAGCTCTCAAGTAACTGCTCT 1484
DB 3057 AATCAAGCTCTCAACCTTATTAATCAAGTAAATCAAGCTCTCAAGTAACTGCTCT 3116
QY 1485 CTCACCTGAGTATTTTCTCTCCCACTTCCCTGCTCTCTCTCTCTCTCTCTCTCT 1544
DB 3117 CTCACCTGAGTATTTTCTCTCCCACTTCCCTGCTCTCTCTCTCTCTCTCTCTCT 3176
QY 1545 TTTGCAAGAGAAATTTTAACATTTTGGGTCCCACTTCAATATGATTAATTAATAC 1604
DB 3177 TTTGCAAGAGAAATTTTAACATTTTGGGTCCCACTTCAATATGATTAATTAATAC 3236
QY 1605 ATTAAGCATTTAATCTCTCTCTCAAGAAATGACAGGCTAAGCATAGCAAAACA 1664
DB 3237 ATTAAGCATTTAATCTCTCTCTCAAGAAATGACAGGCTAAGCATAGCAAAACA 3296
QY 1665 AAGAAATGCTGAGAAATTTGCACTGAGACAGCAATCTGAATTAATTTTCCCAAA 1724
DB 3297 AAGAAATGCTGAGAAATTTGCACTGAGACAGCAATCTGAATTAATTTTCCCAAA 3356
QY 1725 GTTCTTTTATGCTCATATAGTGTGAGATTTGAAGAGCTATTTTATTAATGTTGCA 1784
DB 3357 GTTCTTTTATGCTCATATAGTGTGAGATTTGAAGAGCTATTTTATTAATGTTGCA 3416
QY 1785 CTAGCAACTCATCTTCCGAGAGACAGCAGAGAGATGAAGTGAAGGTTTATA 1844
DB 3417 CTAGCAACTCATCTTCCGAGAGACAGCAGAGAGATGAAGTGAAGGTTTATA 3476
QY 1845 AATCATTTGTAGCAATTAATCCATATATTTTAATCAAGAAATTTGTATATCTT 1904

Db 3477 AATCATTTGTAAGCATTTATCCATATATTATTAATTCAGAAAAATGTTACTT 3536
 Qy 1905 TAGAATTTTGTATCATCTTATATGATAGTACGTCGCTTGAATATAAAG 1964
 Db 3537 TAGAATTTTGTATCATCTTATATGATAGTACGTCGCTTGAATATAAAG 3596
 Qy 1965 ACCAATAATGATCTGTATACCAATCAACATATATTAATATATATATATAC 2024
 Db 3597 ACCAATAATGATCTGTATACCAATCAACATATATATATATATATATATAC 3656
 Qy 2025 ACCCAAAAAAATAAATA 2041
 Db 3657 AAAAAAATAAATAAATA 3673

RESULT 3
 US-10-133-013-103
 ; Sequence 103, Application US/10133013
 ; Publication No. US20030166903A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Astromed, Anna
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Cocks, Benjamin G.
 ; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
 ; FILE REFERENCE: PA-0049 US
 ; CURRENT APPLICATION NUMBER: US/10/133,013
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: 60/287,067
 ; PRIOR FILING DATE: 2001-04-27
 ; NUMBER OF SEQ ID NOS: 271
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 103
 ; LENGTH: 5809
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030166903A1 1330204.51
 US-10-133-013-103

Query Match 95.7%; Score 2001.8; DB 15; Length 5809;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 2029; Conservative 0; Mismatches 2; Indels 16; Gaps 1;

Qy 1 AAGAGACAGACTATTAATCTCCACAGTAAATTAAGACGTATGTCATGTTATTTGTA 60
 Db 3763 AAGAGACAGACTATTAATCTCCACAGTAAATTAAGACGTATGTCATGTTATTTGTA 3822
 Qy 61 AAGAGAGTGAATAGCCTTCAAGCATGTGAATATCTTCATCTTCCCGC----- 111
 Db 3823 AAGCAGTGAATAGCCTTCAAGCATGTGAATATCTTCATCTTCCCGC----- 111
 Qy 112 -----GCTTTTGTGTTCTTTCAGGTAGACACCTTTAAATGACAGAACTAACTGAG 164
 Db 3883 ACAAACAACCTTTTGTGTTCTTTCAGGTAGACACCTTTAAATGACAGAACTAACTGAG 3942
 Qy 165 CATTCAGTAACTTTGCTTCAATCAATTAAGTCAAAATGATGAAAATTTTGTGCC 224
 Db 3943 CATTCAGTAACTTTGCTTCAATCAATTAAGTCAAAATGATGAAAATTTTGTGCC 4002
 Qy 225 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAAATTAATGCTTAAGAT 284
 Db 4003 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAAATTAATGCTTAAGAT 4062
 Qy 285 TCAATGCCAAGAGAACTGTGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 344
 Db 4063 TCAATGCCAAGAGAACTGTGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 4122
 Qy 345 AGCCATGATTTTATTTGTTGATGTGCTCTGTACACAGCCATTTCAATAGATGGA 404
 Db 4123 AGCCATGATTTTATTTGTTGATGTGCTCTGTACACAGCCATTTCAATAGATGGA 4182
 Qy 405 GCTGTAATTAATTTTCAAAAGAGTAATAGACATGCAAAAGTTTCAATAAAACTGGGCA 464

Db 4183 GCTGTAATTAATTTTCAAAAGAGTAATAGACATGCAAAAGTTTCAATAAAACTGGGCA 4242
 Qy 465 TTAAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
 Db 4243 TTAAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4302
 Qy 525 TCAATTAACAATTTGAGATGCTGAAAAGCTAATTAATTTTCAAGAAATGATTTTC 584
 Db 4303 TCAATTAACAATTTGAGATGCTGAAAAGCTAATTAATTTTCAAGAAATGATTTTC 4362
 Qy 585 ATTATTTGAACCTGTTCTCCCTAGCAGGCAATTTTCCCTTTTCCGAGAGTTTACAGT 644
 Db 4363 ATTATTTGAACCTGTTCTCCCTAGCAGGCAATTTTCCCTTTTCCGAGAGTTTACAGT 4422
 Qy 645 TTAGAGAGAAATGATCATGAAAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 704
 Db 4423 TTAGAGAGAAATGATCATGAAAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 4482
 Qy 705 GTAAATGCTCAGACCTATGAAAGCTAATCCCTTTGCTAGAAATTTAAGAGAGCTCAGC 764
 Db 4483 GTAAATGCTCAGACCTATGAAAGCTAATCCCTTTGCTAGAAATTTAAGAGAGCTCAGC 4542
 Qy 765 TTGCTTGAACCTGATTTGTATCTTCATCTTCATTTTGCAGAAAGTATTTTCTGACTGCA 824
 Db 4543 TTGCTTGAACCTGATTTGTATCTTCATCTTCATTTTGCAGAAAGTATTTTCTGACTGCA 4602
 Qy 825 ATGACGCTATGATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 884
 Db 4603 ATGACGCTATGATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4662
 Qy 885 TAAATTTGAGGTTTCTGTCATATCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTCAT 944
 Db 4663 TAAATTTGAGGTTTCTGTCATATCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTCAT 4722
 Qy 945 AATGATATCTTCAACATTCAGACATTCGAAACCCAGAGGTTGGAATTTCTATGAGGT 1004
 Db 4723 AATGATATCTTCAACATTCAGACATTCGAAACCCAGAGGTTGGAATTTCTATGAGGT 4782
 Qy 1005 TTGACATGAATTTGATGATCTTGTATGATTTGATGATTTGATGATTTGATGATTTGAT 1064
 Db 4783 TTGACATGAATTTGATGATCTTGTATGATTTGATGATTTGATGATTTGATGATTTGAT 4842
 Qy 1065 GGTATATGCTCTTCTATCTTATTTAGACAAGACATTTGAAACATTTGTTGCAAGAG 1124
 Db 4843 GGTATATGCTCTTCTATCTTATTTAGACAAGACATTTGAAACATTTGTTGCAAGAG 4902
 Qy 1125 CTCTTATGTTAACAATTTAGACAGTACTGTTTGTGTTAAACACACTTTTCAACCAATAG 1184
 Db 4903 CTCTTATGTTAACAATTTAGACAGTACTGTTTGTGTTAAACACACTTTTCAACCAATAG 4962
 Qy 1185 TTCTGAGCAACGAGAGCAATGACTATTTAAAGAAAGCTTTCCAGCATCACTTAC 1244
 Db 4963 TTCTGAGCAACGAGAGCAATGACTATTTAAAGAAAGCTTTCCAGCATCACTTAC 5022
 Qy 1245 ATCCCAAACTAAAGATCAACTCTTCCAGCTGAGAAAGAAAGCTCTGCTTTGATGGA 1304
 Db 5023 ATCCCAAACTAAAGATCAACTCTTCCAGCTGAGAAAGAAAGCTCTGCTTTGATGGA 5082
 Qy 1305 AACTTACAGAGAGTCAAGGCCAGGCCAACACAGACACAACTTTGAA 1364
 Db 5083 AACTTACAGAGAGTCAAGGCCAGGCCAACACAGACACAACTTTGAA 5142
 Qy 1365 TATTAATTCACATCAGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1424
 Db 5143 TATTAATTCACATCAGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5202
 Qy 1425 AATTCAGCTCTTCAACATTTATACAGTTTAATTAATTAATTAATTAATTAATTAATTAAT 1484
 Db 5203 AATTCAGCTCTTCAACATTTATACAGTTTAATTAATTAATTAATTAATTAATTAATTAAT 5262
 Qy 1485 CTACCTGAGATTTTCTTCCCTCCAGCTTGCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1544

Db	5263	CTACACCTGAGGATATTTTTCCTCCCCACCTGGCCCTGTCCTCCCTCTCTCC	5322
Qy	1545	TTTGCAAGAGGAAATATTTAAACATATTTGGGTCCAACTTCAATATATTAATATAC	1604
Db	5323	TTTCCAAAGAGGAAATATTTAAACATATTTGGGTCCAACTTCAATATATTAATATAC	5382
Qy	1605	ATTAAAAACATTTAATCTCTCTTCTAGAAAAATGACAGGCTTAAGGCAATAGACAAAACA	1664
Db	5383	ATTAAAAACATTTAATCTCTCTTCTAGAAAAATGACAGGCTTAAGGCAATAGACAAAACA	5442
Qy	1665	AGAGAAATGCTGAGAAATTTGCGCACTGGAGACAAGCAATCTGAATAAATATTTGCCAAA	1724
Db	5443	AGAGAAATGCTGAGAAATTTGCGCACTGGAGACAAGCAATCTGAATAAATATTTGCCAAA	5502
Qy	1725	GTTCTTTTATATGTCATATAGTGTCAGATTTGAAGAGACTATTTTTTTTAAATGTTGCA	1784
Db	5503	GTTCTTTTATATGTCATATAGTGTCAGATTTGAAGAGACTATTTTTTTTAAATGTTGCA	5562
Qy	1785	CTAGCAACTCATCTTCGGAAGACACAGCAGCAGAGATAGTAAAGTGAAGGTTTATA	1844
Db	5563	CTAGCAACTCATCTTCGGAAGACACAGCAGCAGAGATAGTAAAGTGAAGGTTTATA	5622
Qy	1845	AATCAATTTGTAAGCAATTTATCCCATATATTTTAAATCAAGAAAAATTTGTTTATCTT	1904
Db	5623	AATCAATTTGTAAGCAATTTATCCCATATATTTTAAATCAAGAAAAATTTGTTTATCTT	5682
Qy	1905	TAGAAATTTGTAATCAATCTTTNGTACATATGCAATGCTCATGCTCTGATTAATTAAGC	1964
Db	5683	TAGAAATTTGTAATCAATCTTTNGTACATATGCAATGCTCATGCTCTGATTAATTAAGC	5742
Qy	1965	ACCAAAATATGATCTGTATACCAACATCATACATATATTAATATATATCTATATAC	2024
Db	5743	ACCAAAATATGATCTGTATACCAACATCATACATATATTAATATATATCTATATAC	5802
Qy	2025	AGCCCAA 2031	
Db	5803	AGCCCAA 5809	
RESULT 4			
US-09-918-715-268			
Sequence 268, Application US/09918715			
Publication No. US20030017157A1			
GENERAL INFORMATION:			
APPLICANT: Brad St. Croix			
APPLICANT: Bert Vogelstein			
APPLICANT: Kenneth Kinzler			
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS			
FILE REFERENCE: 1107.00134			
CURRENT APPLICATION NUMBER: US/09/918.715			
CURRENT FILING DATE: 2001-08-01			
PRIOR APPLICATION NUMBER: 60/222,599			
PRIOR FILING DATE: 2000-08-02			
PRIOR APPLICATION NUMBER: 60/224,360			
PRIOR FILING DATE: 2000-08-11			
PRIOR APPLICATION NUMBER: 60/282,850			
PRIOR FILING DATE: 2000-04-11			
NUMBER OF SEQ ID NOS: 358			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 268			
LENGTH: 1909			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-918-715-268			

	Query Match	89.8%	Score 1878.6	DB 13	Length 1909
	Best Local Similarity	99.7%	Pred. No. 0		
	Matches 1903	Conservative	0	Mismatches 4	Indels 2
QY	134	GACACCTTTTAAATGACAACTAATGAGGATTCCTAGTACTTGGCTTTCAATTCAT	193		
DB	1	GACACCTTTTAAATGACAACTAATGAGGATTCCTAGTACTTGGCTTTCAATTCAT	60		

QY	199	AAAGTCAAAAGTATGAGAAACATTTTGGCCCTATCTCCATACACCCCGGTACTCAAAATTC	253
Db	61	AAAGTCAAAAGTATGAGAAACATTTTGGCCCTACTCTCCATACCCCTGTACTCAAAATTC	120
QY	254	TCTACTGTATGAATTTATGCTTTAAGTAAATTCAGTCCCAAGAGAACTTGGTGAATAA	313
Db	121	TCTACTGTATGAATTTATGCTTTAAGTAAATTCAGTCCCAAGAGAACTTGGTGAATAA	180
QY	314	ATTATTTTAAATTTTTTTTTTATCCTTTACAAAGCAATGGAATTTATTTGGTGTGATG	373
Db	181	ATTATTTTAAATTTTTTTTTTATCCTTTACAAAGCAATGGAATTTATTTGGTGTGATG	240
QY	374	CTCTGTACACAGGCACTTTCATATAGATGAGCGTTAAATTTTCCAAAGATTAATAG	433
Db	241	CTCTGTACACAGGCACTTTCATATAGATGAGCGTTAAATTTTCCAAAGATTAATAG	300
QY	434	ACATGCAAAAGTTTCAATTAATAAACTGGGCCATTACAAATTAATTAATTAATTAAGC	493
Db	301	ACATGCAAAAGTTTCAATTAATAAACTGGGCCATTACAAATTAATTAATTAATTAAGC	360
QY	494	ATTCCCTCTAAGTTTTTGGCCAAACCTGCGTATCCAAATPAACAAATTTGAGATCGTGA	553
Db	361	ATTCCCTCTAAGTTTTTGGCCAAACCTGCGTATCCAAATPAACAAATTTGAGATCGTGA	420
QY	554	AAGCTAGTTATATTTTCAGAGAAATGATTTTCATTTGAATCTGTTCTCCTAGCAGGCC	613
Db	421	AAGCTAGTTATATTTTCAGAGAAATGATTTTCATTTGAATCTGTTCTCCTAGCAGGCC	480
QY	614	ATTTTCCTTTTTCCTGGAGTTTAGACAGTTTAGAGAGAAATAGTCAATGAATAAGAAAG	673
Db	481	ATTTTCCTTTTTCCTGGAGTTTAGACAGTTTAGAGAGAAATAGTCAATGAATAAGAAAG	540
QY	674	GAAGAAAGGGGAGAAGGGAGAAGGTTTAAAAAGTAAGTCTCAGACTTATGAACCTAAATCC	733
Db	541	GAAGAAAGGGGAGAAGGGAGAAGGTTTAAAAAGTAAGTCTCAGACTTATGAACCTAAATCC	600
QY	734	CTTTGCTAGAAATATTTAAGACAGCTCAGCTTGTTGAATCTGAATTTTGTCACTTCC	793
Db	601	CTTTGCTAGAAATATTTAAGACAGCTCAGCTTGTTGAATCTGAATTTTGTCACTTCC	660
QY	794	ATATTGGAGGAAGGTATTTCTGACTGTGCATGCAAGCTATGATGAATAATTTATTTAT	853
Db	661	ATATTGGAGGAAGGTATTTCTGACTGTGCATGCAAGCTATGATGAATAATTTATTTAT	720
QY	854	CATCCTAGAAAGCCTTGAATGAAAAATGAATAAATATGAGGGTTCTGTCCATATCT	913
Db	721	CATCCTAGAAAGCCTTGAATGAAAAATGAATAAATATGAGGGTTCTGTCCATATCT	780
QY	914	GGCTTGCATGTGCCAAGAAAGAGAGATATGAATATGATCCAACTCCAAAGCATGCA	973
Db	781	GGCTTGCATGTGCCAAGAAAGAGAGATATGAATATGATCCAACTCCAAAGCATGCA	840
QY	974	AACCCAAGGGGTAGGCAATCTATGTAGGTTTTGCAATGAATTTGGTGCATCTGGTT	1033
Db	841	AACCCAAGGGGTAGGCAATCTATGTAGGTTTTGCAATGAATTTGGTGCATCTGGTT	900
QY	1034	TATGTGGCTCACTGCTATTAACCTCTCTGGCTTATAGTCTCTTCACTTATTAAGCA	1093
Db	901	TATGTGGCTCACTGCTATTAACCTCTCTGGCTTATAGTCTCTTCACTTATTAAGCA	960
QY	1094	AGCAGGTATCAACACTGTGCTGGCAACAAGGCTTTTATGTTAACAATTTAGACGTACTG	1153
Db	961	AGCAGGTATCAACACTGTGCTGGCAACAAGGCTTTTATGTTAACAATTTAGACGTACTG	1020
QY	1154	TTTGTGTAAACAACCTTTTCAACAATAGGTTCTGAGCAAAAGAGCATATGACTATT	1213
Db	1021	TTTGTGTAAACAACCTTTTCAACAATAGGTTCTGAGCAAAAGAGCATATGACTATT	1080
QY	1214	TAAAGAAAGGTTTCCAGCATCACTTAACAATCCCAAACTTAAATAAATCAACTCTTCC	1273
Db	1081	TAAAGAAAGGTTTCCAGCATCACTTAACAATCCCAAACTTAAATAAATCAACTCTTCC	1144
QY	1274	AACGTAGAAAAGACTCTGGCTTTGAATGAACTTACAGCAGAGATCAAGGCCACGG	1333

[illegible]

NAME/KEY:	CDS	LOCATION:	(69) :	(317)
OTHER INFORMATION:				
US-10-341-434-223				
Query Match	89.8%	Score 1878.6;	DB 16;	Length 1909;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1903;	Conservative	0;	Mismatches	4;
			Indels	2;
			Gaps	2;
QY	134	GACACCTTTTAAATGACAACTACAGAGCATTTGAGTACCTTGCCTTCAATCAAT	193	
DB	1	GACACCTTTTAAATGACAACTACAGAGCATTTGAGTACCTTGCCTTCAATCAAT	60	
QY	194	AAAGTCAAAATGATAGAAACATTTGTGCCCTACTCTCCATACCCCGTGTAAATTC	253	
DB	61	AAAGTCAAAATGATAGAAACATTTGTGCCCTACTCTCCATACCCCGTGTAAATTC	120	
QY	254	TCCTGTAATTAATTAATGCTTGTAGTAAATGAGTCCCAAGAGAACTTGTAATTA	313	
DB	121	TCCTGTAATTAATTAATGCTTGTAGTAAATGAGTCCCAAGAGAACTTGTAATTA	180	
QY	314	ATTATTTTAAATTTTATTTTATTCCTTTACAAAGCCATGATTTTATTTGTTGTGTG	373	
DB	181	ATTATTTTAAATTTTATTTTATTCCTTTACAAAGCCATGATTTTATTTGTTGTGTG	240	
QY	374	CTCTGTACACAGCCATTTCAATGAGATGAGCGTGTAAATTAATTTCCAAAGATATAG	433	
DB	241	CTCTGTACACAGCCATTTCAATGAGATGAGCGTGTAAATTAATTTCCAAAGATATAG	300	
QY	434	ACATGCAAAAGTTTCAATTAATAAATCTGGGCCATTACAAATTAATTAATACTAATAGC	493	
DB	301	ACATGCAAAAGTTTCAATTAATAAATCTGGGCCATTACAAATTAATTAATACTAATAGC	360	
QY	494	ATTCCCTTCTAGTTTTTGGCCAACTGCGCTATCCAAATACAAATTTGAGATCGGTAA	553	
DB	361	ATTCCCTTCTAGTTTTTGGCCAACTGCGCTATCCAAATACAAATTTGAGATCGGTAA	420	
QY	554	AAGCTAGTATTAATTCAGAGAAATGATTTTCATTAATTAATACTGCTCCCTACAGGCC	613	
DB	421	AAGCTAGTATTAATTCAGAGAAATGATTTTCATTAATTAATACTGCTCCCTACAGGCC	480	
QY	614	ATTTTCCCTTTTCTGGAAGTTTACCAAGTTTAGAGAGAAATGCTATGAAAAGAAAG	673	
DB	481	ATTTTCCCTTTTCTGGAAGTTTACCAAGTTTAGAGAGAAATGCTATGAAAAGAAAG	540	
QY	674	GAAAGAAAGGGAAGGGAAGGAGGTTAAAGTAAGTCTCAGACCTATGAAAGTATCC	733	
DB	541	GAAAGAAAGGGAAGGGAAGGAGGTTAAAGTAAGTCTCAGACCTATGAAAGTATCC	600	
QY	734	CTTTCCTAGAAATATTTTAAAGCAGCTCAGCTTGTTGAAACTGAGTTTGTCACTTCC	793	
DB	601	CTTTCCTAGAAATATTTTAAAGCAGCTCAGCTTGTTGAAACTGAGTTTGTCACTTCC	660	
QY	794	AATTTTGCAGAAAGTATTTTCTGACTGCAATGAGTAGATGAAATTTTATTTAT	853	
DB	661	AATTTTGCAGAAAGTATTTTCTGACTGCAATGAGTAGATGAAATTTTATTTAT	720	
QY	854	CATCTCAGAAAGCTTGAATGAAATTAATTAATTTGAGAGGTTTCTGTCCATATCT	913	
DB	721	CATCTCAGAAAGCTTGAATGAAATTAATTAATTTGAGAGGTTTCTGTCCATATCT	780	
QY	914	GCGTTGATGTCACGAAAGCAGAGAAATGAAATGTAATCTCCCAACATCCAAAGATGGA	973	
DB	781	GCGTTGATGTCACGAAAGCAGAGAAATGAAATGTAATCTCCCAACATCCAAAGATGGA	840	
QY	974	AACCCAAAGGATGAGCAATTCATGATAGTTTGGACATGAAGTTTGTCATCTTGATT	1033	
DB	841	AACCCAAAGGATGAGCAATTCATGATAGTTTGGACATGAAGTTTGTCATCTTGATT	900	
QY	1034	TATGTGAGCTCAATGCTATTAACCTCTCTGAGCTTATGCTCTTCATTCATTAATAGCA	1093	
DB	901	TATGTGAGCTCAATGCTATTAACCTCTCTGAGCTTATGCTCTTCATTCATTAATAGCA	960	

QY	1094	AGCAGCGTATCGAAACACTGGCTTCGCAACAAGGCTCTTTAGTTAAACATTTAGAGCTACTG	1153
Dp	961	AGCAGCGTATCGAAACACTGGCTTCGCAACAAGGCTCTTTAGTTAAACATTTAGAGCTACTG	1020
QY	1154	TTTGTGTTAAACACACTTTTCAACCAATPAGTTCTGAGGCACACGAGCAATGACTATTT	1213
Dp	1021	TTTGTGTTAAACACACTTTTCAACCAATPAGTTCTGAGGCACACGAGCAATGACTATTT	1080
QY	1214	TAAAGAAAGGCTTCCGCAACATCTPACACATCCCAAACTAAAGAAATCAACTCTTCC	1273
Dp	1081	TAAAGAAAGGCTTCCGCAACATCTPACACATCCCAAACTAAAGAAATCAACTCTTCC	1140
QY	1274	AACTGAGAAAAGACTCCTGGCTTTGAAATGAAACTTACAGACAGAGTCAAGGCGCAGG	1333
Dp	1141	AACTGAGAAAAGACTCCTGGCTTTGAAATGAAACTTACAGACAGAGTCAAGGCGCAGG	1200
QY	1334	CAACACACAGACACACACAAACATTTGGAAATATATCTCAACCTCAGTTTAATATA	1393
Dp	1201	CAACACACAGACACACACAAACATTTGGAAATATATCTCAACCTCAGTTTAATATA	1260
QY	1394	CATCTT-ATTATTTTCTAGTAGAGAAACTACAAATCAGCCTCTTCAACATTTATATCA	1452
Dp	1261	CATCTTATTTATTTTCTAGTAGAGAACTACAAATCAGCCTCTTCAACATTTATATCA	1320
QY	1453	GTTTAAATAGGCTCTTGCAAGTACTTGTCTCTACCTGAGGATTTTTTTTCCCTCCCA	1512
Dp	1321	GTTTAAATAGGCTCTTGCAAGTACTTGTCTCTACCTGAGGATTTTTTTTCCCTCCCA	1380
QY	1513	CCTTGCCCTGTCTCCCTCTCTCTTCCCTTGGCAAGAGAAATTTTAAACATATTT	1572
Dp	1381	CCTTGCCCTGTCTCCCTCTCTCTTCCCTTGGCAAGAGAAATTTTAAACATATTT	1440
QY	1573	GGGTCCAACTTCAATATATATATTAATATATACATTTAAAGCATTTAACTTCTTCTAGA	1632
Dp	1441	GGGTCCAACTTCAATATATATATTAATATATACATTTAAAGCATTTAACTTCTTCTAGA	1500
QY	1633	AAAAATGCACAGGCTAAGGACATAGACAAACAAAGAGAAATGCTGGAATTTGCCACTGG	1692
Dp	1501	AAAAATGCACAGGCTAAGGACATAGACAAACAAAGAGAAATGCTGGAATTTGCCACTGG	1560
QY	1693	AGACACAGCAATCTGATATAATTTTGCAGAAAGTTCTTTTATGTCAATATAGTGCAGGA	1752
Dp	1561	AGACACAGCAATCTGATATAATTTTGCAGAAAGTTCTTTTATGTCAATATAGTGCAGGA	1620
QY	1753	TTTGAAGAGGCTATTTTTTTTAAATGTGCAACATGCAACCTCATTTGCGAAGACACAGC	1812
Dp	1621	TTTGAAGAGGCTA-TTTTTTTTTAATGTGCAACATGCAACCTCATTTGCGAAGACACAGC	1679
QY	1813	CAGAGAAATGAAGTAGAAGTGAAGGTTTATTAATCATCTTTGTAAAGCATTTATCCCATAT	1872
Dp	1680	CAGAGAAATGAAGTAGAAGTGAAGGTTTATTAATCATCTTTGTAAAGCATTTATCCCATAT	1739
QY	1873	ATTTTAAATTAAGAAAAAATGTGTATACCTTTAAATTTTGATTAATCTTAATGTA	1932
Dp	1740	ATTTTAAATTCAGAAAAAATGTGTATCTTTAATCTTTAATATTTGTATTCATACTTTATGTA	1799
QY	1933	CTATGTGACTCATGCTTCTGATTAATTAAGACACCAAAATATGTATCTGTAAACCAATCA	1992
Dp	1800	CTATGTGACTCATGCTTCTGATTAATTAAGACACCAAAATATGTATCTGTAAACCAATCA	1858
QY	1993	CACATATTAATTAATATATATATCTATATTAACAGCCAAAAAATTTTTTTTTT	2041
Dp	1860	CACATATTAATTAATATATATATCTATATTAACAAAAAATTTTTTTTTT	1908

RESULT 6
US-10-641-643-341
; Sequence 341, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Sellhammer
;

```

1      TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
2      GENE EXPRESSION
3      NUMBER OF SEQUENCES: 1508
4      CORRESPONDENCE ADDRESSES:
5      ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
6      STREET: 3174 PORTER DRIVE
7      CITY: PALO ALTO
8      STATE: CALIFORNIA
9      COUNTRY: USA
10     ZIP: 94304
11
12     COMPUTER READABLE FORM:
13     MEDIUM TYPE: floppy disk
14     COMPUTER: IBM PC compatible
15     OPERATING SYSTEM: PC-DOS/MS-DOS
16     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
17
18     CURRENT APPLICATION DATA:
19     APPLICATION NUMBER: US/10/641,643
20     FILING DATE: 14-Aug-2003
21     CLASSIFICATION: <Unknown>
22
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER: <Unknown>
25     FILING DATE: <Unknown>
26
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Zeller, Karen J
29     REGISTRATION NUMBER: 37,071
30     REFERENCE/DOCKET NUMBER: PA-0001 US
31
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE: (650) 855-0555
34     TELEFAX: (650) 845-4166
35
36     INFORMATION FOR SEQ. ID NO. 341:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 6005 base pairs
39     TYPE: nucleic acid
40     STRANDEDNESS: single
41     TOPOLOGY: linear
42
43     IMMEDIATE SOURCE:
44     LIBRARY: BEPINON01
45     CLONE: 1432736
46
47     SEQUENCE DESCRIPTION: SEQ ID NO: 341 :
48     US-10-641-643-341

```

Query Match	88.6%	Score 1853.4	DB 17	Length 6005
Best Local Similarity	97.2%	Pred. No. 0	Mismatches 27	Indels 32
Matches 2025	Conservative	0		Gaps 13
QY	1	AAGGACAGACTATTAATCTCACAGTAAATTAAGACGTATGTTCCATGTTATTGTTA	60	
Db	3911	AAGGACAGACTTAACTCCACAGTTAATTAAGACGTATGTTCCATGTTATTGTTA	3970	
QY	61	AAGCAGTGTAAAGCCTTCAAGCATGTAAATCTTCCATCTTCCCCGCC-----	112	
Db	3971	AAGCAGTGTAAAGCCTTCAAGCATGTAAATCTTCCATCTTCCCCGCCNNNNNNN	4030	
QY	113	-----GCTTTTGTGTTCTTCAGGTAAACCTTTAAAATGCAGAACTAACTGAG	164	
Db	4031	NNNNNNNNNTTTGTTCTTCAGGTAAACCTTTAAAATGCAGAACTAACTGAGG	4090	
QY	165	CATTTCAGTACTTGTCTTCAANTCAATAAGTCAATGTATGAAACATTTTGTCGC	224	
Db	4091	CATTTCAGTACTTGTCTTCAANTCAATAAGTCAATGTATGAAACATTTTGTCGCC	4150	
QY	225	TACCTTCATACCCCGGTACTCAAAATCTCTACTGATGATGATATGCTTTAATAGAAAT	284	
Db	4151	TACCTTCATACCCCGGTACTCAAAATCTCTACTGATGATGATATGCTTTAATAGAAAT	4210	
QY	285	TCAGTGCAAGAGAACTGTGTGAATAAATTATTTTAA-TTTTTTTTTATCCTTTACA	343	
Db	4211	TCAGTGCAAGAGAACTGTGTGAATAAATTATTTTAA-TTTTTTTTTATCCTTTACA	4270	
QY	344	AAGCAGATTTTATTGTTGATGTGTCCTCTGTACAAAGCATTTTCAATGTAGATG	403	
Db	4271	AAGCAGATTTTATTGTTGATGTGTCCTCTGTACAAAGCATTTTCAATGTAGATG	4330	

Thu May 6 14:19:49 2004

us-09-646-569a-60.rmp

Page 9

Query Match 22.6%; Score 472.8; DB 13; Length 500;
Best Local Similarity 99.2%; Pred. No. 2e-97;
Matches 485; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1279 AGAAGAACTCTGCTTGAATGAACTTACAGCAGAGATCAGGCGCAGGCAACA 1338
12 AAAAGAACTCTGCTTGAATGAACTTACAGCAGAGATCAGGCGCAGGCAACA 71
1339 ACAAGCAACAACAACATTTGAAATATTCTCACTCAGCTTTTAAATACATCT 1398
72 ACAAGCAACAACAACATTTGAAATATTCTCACTCAGCTTTTAAATACATCT 131
1399 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTTATATACATTTA 1458
132 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTTATATACATTTA 191
1459 TAAAGCTCTTGAAGTACTTCTCTCACTGAGTATTTTCTCCCGACCTTGC 1518
192 TAAAGCTCTTGAAGTACTTCTCTCACTGAGTATTTTCTCCCGACCTTGC 251
1519 CCTGTCTCTGCT 1578
252 CCTGTCTCTGCT 311
1579 AACTCAAT 1637
312 AACTCAAT 371
1638 GCACAGGCTTAAGGCTATAGCAAAAACAAAGAGAAATGCTGAGAAATTTGCCA 1697
372 GCACAGGCTTAAGGCTATAGCAAAAACAAAGAGAAATGCTGAGAAATTTGCCA 431
1698 AGCAATCTGAATTAATATTTTGCAGAAAGTCTTTTATATATATATATATATAT 1757
432 AGCAATCTGAATTAATATTTTGCAGAAAGTCTTTTATATATATATATATATAT 491
1758 AGAGACTAT 1766
492 AGAGACTAT 500

RESULT 8

US-10-242-535A-24331
Sequence 24331, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24331
LENGTH: 500
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(11)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(18)

OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-24331

Query Match 22.6%; Score 472.8; DB 16; Length 500;
Best Local Similarity 99.2%; Pred. No. 2e-97;
Matches 485; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

1279 AGAAGAACTCTGCTTGAATGAACTTACAGCAGAGATCAGGCGCAGGCAACA 1338
12 AAAAGAACTCTGCTTGAATGAACTTACAGCAGAGATCAGGCGCAGGCAACA 71
1339 ACAAGCAACAACAACATTTGAAATATTCTCACTCAGCTTTTAAATACATCT 1398
72 ACAAGCAACAACAACATTTGAAATATTCTCACTCAGCTTTTAAATACATCT 131
1399 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTTATATACATTTA 1458
132 TATTATTTTCTAGTAGAGAACTACAAATCAGCTCTTCACTTTATATACATTTA 191
1459 TAAAGCTCTTGAAGTACTTCTCTCACTGAGTATTTTCTCCCGACCTTGC 1518
192 TAAAGCTCTTGAAGTACTTCTCTCACTGAGTATTTTCTCCCGACCTTGC 251
1519 CCTGTCTCTGCT 1578
252 CCTGTCTCTGCT 311
1579 AACTCAAT 1637
312 AACTCAAT 371
1638 GCACAGGCTTAAGGCTATAGCAAAAACAAAGAGAAATGCTGAGAAATTTGCCA 1697
372 GCACAGGCTTAAGGCTATAGCAAAAACAAAGAGAAATGCTGAGAAATTTGCCA 431
1698 AGCAATCTGAATTAATATTTTGCAGAAAGTCTTTTATATATATATATATATAT 1757
432 AGCAATCTGAATTAATATTTTGCAGAAAGTCTTTTATATATATATATATATAT 491
1758 AGAGACTAT 1766
492 AGAGACTAT 500

RESULT 9

US-10-085-783A-36782
Sequence 36782, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36782
LENGTH: 466
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(15)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature

LOCATION: (43)..(43)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-36782

Query Match 21.0%; Score 439.6; DB 13; Length 466;
Best Local Similarity 98.7%; Pred. No. 7.1e-90;
Matches 442; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

973 AAACCCAGGGGTAGGCAATTCTATAGTGTGGACATGAAGTTGGTGCATCTTGT 1032
14 ANCCCAAGGGGTAGGCAATTCTATAGTGTGGACATGAAGTTGGTGCATCTTGT 73
1033 TTAATGCTGCTCACTGCTATTAACCTCTGGCTTAATGCTCTTCACTTCTATTAG 1092
74 TTAATGCTGCTCACTGCTATTAACCTCTGGCTTAATGCTCTTCACTTCTATTAG 133
1093 AAGCAGTATCGAACCTTGTGCGACAAGGCTCTTATAGTAACAATTAGCAGCTACT 1152
134 AAGCAGTATCGAACCTTGTGCGACAAGGCTCTTATAGTAACAATTAGCAGCTACT 193
1153 GTTGTGTTAAACACTTTTCAACCAATAGTTCTGAGGCAACGAGGCAATGACTAT 1212
194 GTTGTGTTAAACACTTTTCAACCAATAGTTCTGAGGCAACGAGGCAATGACTAT 253
1213 TTAAGAAAGGCTTCCAGCATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 1272
254 TTAAGAAAGGCTTCCAGCATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 313
1273 CACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 1332
314 CACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 373
1333 GCAACAACAACAACAACAACAACAATTGGAAATATTCTCACTCAGCTTTATAT 1392
374 GCAACAACAACAACAACAACAACAATTGGAAATATTCTCACTCAGCTTTATAT 433
1393 ACATCTTATTATTTTCTAGTAGAGAA 1420
434 ACATCTTATTATTTTCTAGTAGAGAA 461

RESULT 10

US-10-242-535A-36782
Sequence 36782, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/085,783
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36782
LENGTH: 466
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (43)..(43)

OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-36782

Query Match 21.0%; Score 439.6; DB 16; Length 466;
Best Local Similarity 98.7%; Pred. No. 7.1e-90;
Matches 442; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

973 AAACCCAGGGGTAGGCAATTCTATAGTGTGGACATGAAGTTGGTGCATCTTGT 1032
14 ANCCCAAGGGGTAGGCAATTCTATAGTGTGGACATGAAGTTGGTGCATCTTGT 73
1033 TTAATGCTGCTCACTGCTATTAACCTCTGGCTTAATGCTCTTCACTTCTATTAG 1092
74 TTAATGCTGCTCACTGCTATTAACCTCTGGCTTAATGCTCTTCACTTCTATTAG 133
1093 AAGCAGTATCGAACCTTGTGCGACAAGGCTCTTATAGTAACAATTAGCAGCTACT 1152
134 AAGCAGTATCGAACCTTGTGCGACAAGGCTCTTATAGTAACAATTAGCAGCTACT 193
1153 GTTGTGTTAAACACTTTTCAACCAATAGTTCTGAGGCAACGAGGCAATGACTAT 1212
194 GTTGTGTTAAACACTTTTCAACCAATAGTTCTGAGGCAACGAGGCAATGACTAT 253
1213 TTAAGAAAGGCTTCCAGCATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 1272
254 TTAAGAAAGGCTTCCAGCATCACTTACACATCCCAAACTTAAAGATCAACTCTTC 313
1273 CACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 1332
314 CACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACG 373
1333 GCAACAACAACAACAACAACAACAATTGGAAATATTCTCACTCAGCTTTATAT 1392
374 GCAACAACAACAACAACAACAACAATTGGAAATATTCTCACTCAGCTTTATAT 433
1393 ACATCTTATTATTTTCTAGTAGAGAA 1420
434 ACATCTTATTATTTTCTAGTAGAGAA 461

RESULT 11

US-10-085-783A-20216
Sequence 20216, Application US/10085783A
Publication No. US2004003784LAI
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20216
LENGTH: 460
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (120)..(120)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (301)..(301)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-20216

Query Match 18.6%; Score 389.8; DB 13; Length 460;
 Best Local Similarity 97.0%; Pred. No. 1.6e-78;
 Matches 449; Conservative 0; Mismatches 9; Indels 5; Gaps 5;

1428 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 1486
 1 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 60
 1487 CACCTGAGGATTTTCTTCCCTCCCACTTGGCCCTGTCTCTCTCTCTCTCTCT 1546
 61 CACCTGAGGATTTTCTTCCCTCCCACTTGGCCCTGTCTCTCTCTCTCTCTCT 120
 1547 TCGAAGAGAAATATTTAATTAATTTGGGTCCCACTTCAATATATATATATACAT 1606
 121 TCGAAGAGAAATATTTAATTAATTTGGGTCCCACTTCAATATATATATATACAT 180
 1607 T-AAAAGCATTTAACTCTCTCTCTGAGAAAATGCAAGGCTAAGGCAATAGCAAAA 1665
 181 TAAAAGCATTTAACTCTCTCTCTGAGAAAATGCAAGGCTAAGGCAATAGCAAAA 240
 1666 GAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCTGAATTAATTTGCCAAA 1725
 241 GAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCTGAATTAATTTGCCAAA 300
 1726 TTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTATATGTGCAAC 1785
 301 NTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTATATGTGCAAC 360
 1786 TAGCACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTAAGTAAGTAAGTTTAA 1845
 361 TAGCACTCATCTTGGAGAGAGCCAGAGAAATGAAGTAAGTAAGTAAGTTTAA 418
 1846 ATCCATTGTGAAGCATTTATCCCATATATTTTAAATTCAGAA 1888
 419 ATCCATTGTGAAGC-TTATATCAATATATTTTAAATTCAGAA 460

RESULT 12
 US-10-242-535A-20216
 / Sequence 20216, Application US/10242535A
 / Publication No. US20040013663A1
 / GENERAL INFORMATION:
 / APPLICANT: ChondroGene Inc.
 / APPLICANT: Liew, C.C.
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 / FILE REFERENCE: 4231/2005
 / CURRENT APPLICATION NUMBER: US/10/242,535A
 / CURRENT FILING DATE: 2002-09-12
 / PRIOR APPLICATION NUMBER: US 10/085,783
 / PRIOR FILING DATE: 2002-02-28
 / PRIOR APPLICATION NUMBER: US 60/305,340
 / PRIOR FILING DATE: 2001-07-13
 / PRIOR APPLICATION NUMBER: US 60/275,017
 / PRIOR FILING DATE: 2001-03-12
 / PRIOR APPLICATION NUMBER: US 60/271,955
 / PRIOR FILING DATE: 2001-02-28
 / NUMBER OF SEQ ID NOS: 58994
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 20216
 / LENGTH: 460
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (120)..(120)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (301)..(301)
 / OTHER INFORMATION: n is a, c, g, or t
 / US-10-242-535A-20216

Query Match 18.6%; Score 389.8; DB 16; Length 460;

Best Local Similarity 97.0%; Pred. No. 1.6e-78;
 Matches 449; Conservative 0; Mismatches 9; Indels 5; Gaps 5;

1428 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 1486
 1 TCAGCCTCTTCAACATTTATATACAGTTTAAAGCCCTTGAAGTTA-CTTGTCTCT 60
 1487 CACCTGAGGATTTTCTTCCCTCCCACTTGGCCCTGTCTCTCTCTCTCTCTCT 1546
 61 CACCTGAGGATTTTCTTCCCTCCCACTTGGCCCTGTCTCTCTCTCTCTCTCT 120
 1547 TCGAAGAGAAATATTTAATTAATTTGGGTCCCACTTCAATATATATATATACAT 1606
 121 TCGAAGAGAAATATTTAATTAATTTGGGTCCCACTTCAATATATATATATATACAT 180
 1607 T-AAAAGCATTTAACTCTCTCTCTGAGAAAATGCAAGGCTAAGGCAATAGCAAAA 1665
 181 TAAAAGCATTTAACTCTCTCTCTGAGAAAATGCAAGGCTAAGGCAATAGCAAAA 240
 1666 GAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCTGAATTAATTTGCCAAA 1725
 241 GAGAAATGCTGAGAAATTTGCCACTGAGAGACAGCAATCTGAATTAATTTGCCAAA 300
 1726 TTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTATATGTGCAAC 1785
 301 NTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTATATGTGCAAC 360
 1786 TAGCACTCATCTTGGAGAGACAGCCAGAGAAATGAAGTAAGTAAGTAAGTTTAA 1845
 361 TAGCACTCATCTTGGAGAGAGCCAGAGAAATGAAGTAAGTAAGTAAGTTTAA 418
 1846 ATCCATTGTGAAGCATTTATCCCATATATTTTAAATTCAGAA 1888
 419 ATCCATTGTGAAGC-TTATATCAATATATTTTAAATTCAGAA 460

RESULT 13
 US-10-085-783A-22085
 / Sequence 22085, Application US/10085783A
 / Publication No. US20040037841A1
 / GENERAL INFORMATION:
 / APPLICANT: ChondroGene Inc.
 / APPLICANT: Liew, C.C.
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 / FILE REFERENCE: 4231/2002
 / CURRENT APPLICATION NUMBER: US/10/085,783A
 / CURRENT FILING DATE: 2002-02-28
 / PRIOR APPLICATION NUMBER: US 60/305,340
 / PRIOR FILING DATE: 2001-07-13
 / PRIOR APPLICATION NUMBER: US 60/275,017
 / PRIOR FILING DATE: 2001-03-12
 / PRIOR APPLICATION NUMBER: US 60/271,955
 / PRIOR FILING DATE: 2001-02-28
 / NUMBER OF SEQ ID NOS: 58994
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 22085
 / LENGTH: 400
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (41)..(41)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (64)..(65)
 / OTHER INFORMATION: n is a, c, g, or t
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (215)..(216)
 / OTHER INFORMATION: n is a, c, g, or t
 / US-10-085-783A-22085

Query Match	17.4%	Score 364;	DB 13;	Length 400;
Best Local Similarity	97.2%	Pred. No. 1.1e-72;		
Matches 378; Conservative	0;	Mismatches 10;	Indels 1;	Gaps 1;

QY	134	AAACAACAACATTGGATATATATATCTCAACCTCAGCTTTAAATACATCTTAATATT	1406
Db	12	MACCCAACATTGGATATATATCTTTCCTCAGCTTTAAATACATCTTNTATATT	71
QY	1407	TTCTAGTAGAGAACTACCAATCAGCTCTTCAACATTTAATACAGTTTAATTAAGCTC	1466
Db	72	TTCTAGTAGAGAACTACCAATCAGCTCTTCAACATTTAATACAGTTTAATTAAGCTC	131
QY	1467	TTTGCAAGTACTTGTCTCTCACCCTGAGGTATTTTTTCTCCCACTGGCCCGTTC	1526
Db	132	TTTGCAAGTACTGTCTCTCTCACCCTGAGGTATTTTTTCTCCCACTGGCCCGTTC	191
QY	1527	CTCCCTTCCTCTTCCTCCCTTGACAGAGAAATATTAAATATTGGGTCAACTTCAA	1586
Db	192	CTCCCTTCCTCTTCCTCCCTTGACAGAGAAATATTAAATATTGGGTCAACTTCAA	251
QY	1587	TAAATGTAATTAATTAATACATT-AAAAAGATTAACTTCTTGAGAAAATGCAAGGC	164
Db	252	TAAATGTAATTAATTAATACATTAAAAAGATTAACTTCTTGAGAAAATGCAAGGC	311
QY	1646	TAAAGCATATGACAAAACAAAGAGAAATCTGAGAAATTTGCCACTGAGACAAAGCAATCT	170
Db	312	TAAAGCATATGACAAAACAAAGAGAAATCTGAGAAATTTGCCACTGAGACGAGCAATCT	371
QY	1706	GAATTAATATTTGGCAAAAGTCTCTTTTA	1734
Db	372	GAATTAATATTTGGCAAAAGTCTCTTTTA	400

RESULT 14
US-10-242-535A-22085
Sequence 22085, Application US/10242535A
Publication No. US2004001363A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

Query Match 17.4%; Score 364; DB 16; Length 400;

Best Local Similarity 97.2%; Pred. No. 1.1e-72;
Matches 378; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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QY	1407	TTCTAGTAGAGAAACTACAAATCAGCCTCTTCAACATTTATATACAGTTTATATAGCCTC	1466
Db	72	TTCTAGTAGAGAAACTACAAATCAGCCTCTTCAACATTTATATACAGTTTATATAGCCTC	131
QY	1467	TTTGCAATTACTGTGTCTCTCACTGAGATATTTTTTTCCTCCCACTGCGCCTGTCTC	1526
Db	132	TTTGCAATTACTGTGTCTCTCACTGAGATATTTTTTTCCTCCCACTGCGCCTGTCTC	191
QY	1527	CTCCCTTCCTCTTCCTCCTTTGCAAGAGAAATTTAAATATTTGGGTCAACTTCAA	1586
Db	192	CTCCCTTCCTCTTCCTCCTTTGCAAGAGAAATTTAAATATTTGGGTCAACTTCAA	251
QY	1587	TAATGTATATATTAATATCAATT-AAAAGCAATTAACTTCCTTTCTAGAAAAATGACAGGC	1645
Db	252	TAATGTATATATTAATATCAATTAAAAACATTTAACTTCCTTTCTAGAAAAATGACAGGC	311
QY	1646	TAAGGCATTAACAACAAACAAGAGAAATGCTGAGAAATTTGGCACTGGAGACAACAATCT	1705
Db	312	TAAGGCATTAACAACAAACAAGAGAAATGCTGAGAAATTTGGCACTGGAGAGACAACAATCT	371
QY	1706	GAATTAATATTTGGCAAAAGTTCTTTTAA	1734
Db	372	GAATTAATATTTGGCAAAAGTTCTTTTAA	400

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Best Local Similarity	100.0%;	Pred. No. 3.2e-65;		

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QY	1758	AGGAGCTATTTTTTTTATATGTTGCACTAGCAACTCATCTTCGGAAGACACAGCCAGGA	1817							
Db	271	AGGAGCTATTTTTTTTATATGTTGCACTAGCAACTCATCTTCGGAAGACACAGCCAGGA	212							
QY	1818	GAATGAGTAGAAGTGAAGGTTTATAATCCATTGTAGCAATTATCCCATATATTTT	1877							
Db	211	GAATGAGTAGAAGTGAAGGTTTATAATCCATTGTAGCAATTATCCCATATATTTT	152							
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Db	151	AAATTCAGAAAAAATGTTTATCTTTAGAAATTTTGATTCATTAATCTTATGTAATG	92							
QY	1938	TGACTCATGCTTCTGATTAATAAAGCACCAAAATATGTCTGTACCACATCACACAT	1997							
Db	91	TGACTCATGCTTCTGATTAATAAAGCACCAAAATATGTCTGTACCACATCACACAT	32							
QY	1998	ATTATATTAAATATATATCTATATACGCC	2028							
Db	31	ATTATATTAAATATATATCTATATACGCC	1							

Search completed: May 6, 2004, 03:11:12
Job time : 868 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 14:13:19 ; Search time 154 Seconds

(without alignments)
7535.080 Million cell updates/sec

Title: US-09-646-569a-60

Perfect score: 2091 1 aagagacacacatactac.....ggagagagggggggaggt 2091

Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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6: /cgn2_6/prodata/2/ina/Backfill1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2003.8	95.8	3674	4	US-09-482-273-73 Sequence 73, Appl
2	1853.4	88.6	6005	4	US-09-023-655-141 Sequence 341, App
3	65.4	3.1	301	4	US-09-439-313-280 Sequence 280, App
4	65.4	3.1	301	4	US-09-352-616A-280 Sequence 280, App
5	65.4	3.1	301	4	US-09-232-149A-280 Sequence 280, App
6	65.4	3.1	301	4	US-09-159-812-280 Sequence 280, App
7	65.4	3.1	301	4	US-09-636-215-280 Sequence 280, App
8	65.4	3.1	301	4	US-09-685-166A-280 Sequence 280, App
9	65.4	3.1	301	4	US-09-688-489-280 Sequence 280, App
10	54.4	2.6	2447	2	US-09-014-962-14 Sequence 14, Appl
11	51.4	2.5	832	4	US-09-621-976-2813 Sequence 2813, Ap
12	50.2	2.4	7218	1	US-08-232-463-14 Sequence 14, Appl
13	48.8	2.3	1559	4	US-09-489-847-42 Sequence 42, Appl
14	48.4	2.3	169998	4	US-09-676-610B-24 Sequence 24, Appl
15	48.4	2.3	197496	4	US-09-877-177A-10 Sequence 10, Appl
16	47.6	2.3	1664976	4	US-08-916-421B-1 Sequence 1, Appl
17	47.4	2.3	1810	4	US-09-800-723-72 Sequence 72, Appl
18	47.4	2.3	1811	4	US-09-800-723-77 Sequence 77, Appl
19	47.2	2.3	593	4	US-09-904-615-59 Sequence 59, Appl
20	46.8	2.2	1641	1	US-08-903A-8 Sequence 8, Appl
21	46.8	2.2	1641	4	US-08-988-197-8 Sequence 8, Appl
22	46.6	2.2	6669	4	US-10-204-708-5 Sequence 5, Appl
23	46.4	2.2	3527	2	US-08-909-965C-7 Sequence 7, Appl
24	46.4	2.2	7218	1	US-08-232-463-14 Sequence 14, Appl
25	46.2	2.2	12141	3	US-09-488-671-10 Sequence 10, Appl
26	45.6	2.2	6124	3	US-08-213-415B-3 Sequence 3, Appl
27	45.6	2.2	6669	4	US-10-204-708-6 Sequence 6, Appl

28	45.2	2.2	1051	3	US-09-245-041-10 Sequence 10, Appl
29	44.8	2.1	731	1	US-08-451-405A-2 Sequence 2, Appl
30	44.6	2.1	2230	3	US-08-378-313-24 Sequence 24, Appl
31	44.6	2.1	5152	4	US-10-204-708-73 Sequence 73, Appl
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35	44.4	2.1	1150	4	US-09-390-207-1 Sequence 1, Appl
36	44.4	2.1	2485	4	US-09-889-463A-9 Sequence 9, Appl
37	44.4	2.1	53332	4	US-09-801-861-3 Sequence 64, Appl
38	44.2	2.1	1361	4	US-09-489-847-64 Sequence 64, Appl
39	43.8	2.1	664	4	US-09-594-506-37 Sequence 37, Appl
40	43.8	2.1	2280	3	US-08-813-150-1 Sequence 1, Appl
41	43.8	2.1	2280	4	US-09-546-553-1 Sequence 1, Appl
42	43.6	2.1	2406	4	US-09-594-506-37 Sequence 37, Appl
43	43.4	2.1	1141	4	US-09-800-723-78 Sequence 78, Appl
44	43.4	2.1	3812	4	US-09-784-316-1 Sequence 1, Appl
45	43.4	2.1	5852	1	US-07-867-106-2 Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-482-273-73
Sequence 73, Application US/09482273
Parent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentm Ver. 2.0
SEQ ID NO 73
LENGTH: 3674
TYPE: DNA
ORGANISM: Homo sapiens
US-09-482-273-73
Query Match 95.8%; Score 2003.8; DB 4; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2034; Conservative 7; Indels 16; Gaps 1;
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1737 ACACACACACTTTTGTGTTTCAAGTGAATATCTTCATTTCCCGC-----1796
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1857 TACTTCACATACCCCGGTGCTCAATCTTCATTTCCCGC-----1916
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QY 285 TCAGTCCAGAGAGAACTGGTGAATATAATTATTATTTTCTTAACTTACAA 344
DB 1917 TCAGTCCAGAGAGAACTGGTGAATATAATTATTATTTTCTTAACTTACAA 1976
QY 345 AGCCATGATATTTATTTGGTGTGATGTGCTGTGACAGACCATTCATAGATGGA 404
DB 1977 AGCCATGATATTTATTTGGTGTGATGTGCTGTGACAGACCATTCATAGATGGA 2036
QY 405 GCTGTATATTTATTTCCAAAGAGTATAGCATGCAAGAAAGTTTCAATAAATCTGGGCA 464
DB 2037 GCTGTATATTTATTTCCAAAGAGTATAGCATGCAAGAAAGTTTCAATAAATCTGGGCA 2096
QY 465 TTACAAATTAATTAATACTAATAGCAATTCCTCTTAGGTTTTCGCAACTGCCTA 524
DB 2097 TTACAAAGTAAATTAATACTAATAGCAATTCCTCTTAGGTTTTCGCAACTGCCTA 2156
QY 525 TCCAAATTAATAATTTGAGATCGTTGAAAAGTACTATTTTACAGAGAAATGATTTTC 584
DB 2157 TCCAAATTAATAATTTGAGATCGTTGAAAAGTACTATTTTACAGAGAAATGATTTTC 2216
QY 585 ATTATTAATACTGTCTCCCTAGCAGGCAATTTCCCTTTTCTGGGAGTTTACAGAT 644
DB 2217 ATTATTAATACTGTCTCCCTAGCAGGCAATTTCCCTTTTCTGGGAGTTTACAGAT 2276
QY 645 TTGAGAGAGATATGTCATGAAAAGAAAGGAAAGGGAAGAGGAAAGAGTTTAAAA 704
DB 2277 TTGAGAGAGATATGTCATGAAAAGAAAGGAAAGGGAAGAGGAAAGAGTTTAAAA 2336
QY 705 GTAGAGTCTCAGACCTATGACGTATCCCTTTGCTAGAAATATTTAAGACAGCTCAGC 764
DB 2337 GTAGAGTCTCAGACCTATGACGTATCCCTTTGCTAGAAATATTTAAGACAGCTCAGC 2396
QY 765 TTGCTTGAACCTGAGTTTGTCTCATCTTCCATATTTGACAGAAAGATTTTCTGACTGCA 824
DB 2397 TTGCTTGAACCTGAGTTTGTCTCATCTTCCATATTTGACAGAAAGATTTTCTGACTGCA 2456
QY 825 ATGCAGCTAGATGTAATTTTATTTTATCATCCCTAGAAAGCCTGACAGAAATATAA 884
DB 2457 ATGCAGCTAGATGTAATTTTATTTTATCATCCCTAGAAAGCCTGACAGAAATATAA 2516
QY 885 TAAATATGAGGTTTCTGTCCATATCTGGCTTGATGTCAGAAAGCAGAGATAGA 944
DB 2517 TAAATATGAGGTTTCTGTCCATATCTGGCTTGATGTCAGAAAGCAGAGATAGA 2576
QY 945 AAATGTAATCTCCAAATCCAGACATCCAAACCCAGGGGTAGCAATTTCTATGAGTT 1004
DB 2577 AAATGTAATCTCCAAATCCAGACATCCAAACCCAGGGGTAGCAATTTCTATGAGTT 2636
QY 1005 TTGAGCATGAGTTTGTGATCTTGTATGCTGCTCAACTGCTATTAACCTCTCT 1064
DB 2637 TTGAGCATGAGTTTGTGATCTTGTATGCTGCTCAACTGCTATTAACCTCTCT 2696
QY 1065 GGGTTATAGTCTCTTATTTATTTAGACAAGCAGTATGAAACCTTGTGCAAGG 1124
DB 2697 GGGTTATAGTCTCTTATTTATTTAGACAAGCAGTATGAAACCTTGTGCAAGG 2756
QY 1125 CTCTTAGTTAACTATTTAGACAGTCTTTGTTGTTAAACAACCTTTCACTAATAGG 1184
DB 2757 CTCTTAGTTAACTATTTAGACAGTCTTTGTTGTTAAACAACCTTTCACTAATAGG 2816
QY 1185 TTCTGAGGCAAGAGAGCATGACTATTTAAAGAAAGGCTTCCAGCATCACTTAAC 1244
DB 2817 TTCTGAGGCAAGAGAGCATGACTATTTAAAGAAAGGCTTCCAGCATCACTTAAC 2876
QY 1245 ATCCCAAACTAAAAAGATCACTCTTCCACGTAAGAAAGACTCTGGCTTTGATGGA 1304
DB 2877 ATCCCAAACTAAAAAGATCACTCTTCCACGTAAGAAAGACTCTGGCTTTGATGGA 2936
QY 1305 AACTTAACAGAGAGTCAAGGCGCAAGCAACACAGCAACAAACATTTGGA 1364
DB 2937 AACTTAACAGAGAGTCAAGGCGCAAGCAACACAGCAACAAACATTTGGA 2996
QY 1365 TATATTCCTCACTCAGTTTAAATATGATCTTATTTTCTAGTAGAGAAACATAC 1424

DB 2997 TATATTCCTCACTCAGTTTAAATATGATCTTATTTTCTAGTAGAGAACTAC 3056
QY 1425 AAATCAGCTCTTCAACATTTATATACAGTTTAAAGCTCTTGCAGTACTTGTCT 1484
DB 3057 AAATCAGCTCTTCAACATTTATATACAGTTTAAAGCTCTTGCAGTACTTGTCT 3116
QY 1485 CTCACCTGAGTATTTTCTCCCTCCAGCTCTGCTGCTCTCTCTCTCTCTCTCTCT 1544
DB 3117 CTCACCTGAGTATTTTCTCCCTCCAGCTCTGCTGCTCTCTCTCTCTCTCTCTCT 3176
QY 1545 TTGCAAGAGCAATATTTAATATTTGAGTCACTTGGTCACTTCAATATATATATATAC 1604
DB 3177 TTGCAAGAGCAATATTTAATATTTGAGTCACTTGGTCACTTCAATATATATATATAC 3236
QY 1605 ATTAAAGCATTTTACTCTCTCTTCTGAAAAGTCAAGCTAAGGCATAGACAAACAA 1664
DB 3237 ATTAAAGCATTTTACTCTCTCTTCTGAAAAGTCAAGCTAAGGCATAGACAAACAA 3296
QY 1665 AGAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATATTTGCCAAA 1724
DB 3297 AGAGAAATGCTGAGAAATTTGCCACTGAGACAGCAATCTGAATAATATTTGCCAAA 3356
QY 1725 GTTCTTTTATATGATATATGTCAGAGATTTGAAAGAGCTATTTTAAATAGTGCA 1784
DB 3357 GTTCTTTTATATGATATATGTCAGAGATTTGAAAGAGCTATTTTAAATAGTGCA 3416
QY 1785 CTAGCAATCATCTTGGAGAGACAGCCAGAGAAATGAGTGAAGTGAAGGTTTATA 1844
DB 3417 CTAGCAATCATCTTGGAGAGACAGCCAGAGAAATGAGTGAAGTGAAGGTTTATA 3476
QY 1845 AATCATTGTTAGCATTTATCCCATATATTTTAAATTCAGAAATATGTTTATCTT 1904
DB 3477 AATCATTGTTAGCATTTATCCCATATATTTTAAATTCAGAAATATGTTTATCTT 3536
QY 1905 TAGAATTTGATTCATATCTTATGATGATGATGATGATGATGATGATGATGATGAT 1964
DB 3537 TAGAATTTGATTCATATCTTATGATGATGATGATGATGATGATGATGATGATGAT 3596
QY 1965 ACCAATATATATGATGTAACCAACATGACATATTAATATATATATATATATATAC 2024
DB 3597 ACCAATATATATGATGTAACCAACATGACATATTAATATATATATATATATATAC 3556
QY 2025 AGCCAAAAAATAAAAA 2041
DB 3657 AAAAAAATAAAAA 3673

RESULT 2
US-09-023-655-341
Sequence 341, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Selhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREMITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 341:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6005 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BEPINON01
 CLONE: 1432736
 US-09-023-655-341

Query Match 88.6%; Score 1853.4; DB 4; Length 6005;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 2025; Conservative 0; Mismatches 27; Indels 32; Gaps 13;

QY 1 AAGAGACGACTTAACTCCACAGTTTAAAGAGGTATGTTCCATGTTTATTGTTA 60
 DB 3911 AAGAGACGACTTAACTCCACAGTTTAAAGAGGTATGTTCCATGTTTATTGTTA 3970
 QY 61 AAGAGGTGTAATGCTTCAAGCATGTAATATCTCCATCTTCCCGCC----- 112
 DB 3971 AAGAGGTGTAATGCTTCAAGCATGTAATATCTCCATCTTCCCGCCNNNNNNNN 4030
 QY 113 -----GCTTTTGTTCCTTCAAGTACACCTTTTAAATGCACTAACTAGG 164
 DB 4031 NNNNNNNNNNTTGTTCCTTCAAGTACACCTTTTAAATGCACTAACTAGG 4090
 QY 165 CATTTCAGTACTTGTCTTCAATCAATAAGTCAATGTAAGAAATTTTGTGCCC 224
 DB 4091 CATTTCAGTACTTGTCTTCAATCAATAAGTCAATGTAAGAAATTTTGTGCCC 4150
 QY 225 TACTCTCCATACCCCGTACTCAATCTCTACTGTAATGTAATGTTTAACTAGTAA 284
 DB 4151 TACTCTCCATACCCCGTACTCAATCTCTACTGTAATGTAATGTTTAACTAGTAA 4210
 QY 285 TCAGTGCAGAGAGACTTGTGAATTAATTTTAA-TTTTTTTTTATCCTTTACA 343
 DB 4211 TCAGTGCAGAGAGACTTGTGAATTAATTTTAA-TTTTTTTTTATCCTTTACA 4270
 QY 344 AAGCATGATTTTATTTGTTGATGTTGCTGTGTACACAAGCATTTCAATAGATG 403
 DB 4271 AAGCATGATTTTATTTGTTGATGTTGCTGTGTACACAAGCATTTCAATAGATG 4330
 QY 404 AGCTGTAAATTTTCCAAAGAGTAATAGACATGCAAAAGTTTCAATATAAACTGGCC 463
 DB 4331 AGCTGTAAATTTTCCAAAGAGTAATAGACATGCAAAAGTTTCAATATAAACTGGCC 4390
 QY 464 AATTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 523
 DB 4391 AATTAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4450
 QY 524 ATCCATTAACAATAATTTGAAGATGTTGAAAAAGCTAGTATATTTCAAGAAATGATTT 583
 DB 4451 ATCCATTAACAATAATTTGAAGATGTTGAAAAAGCTAGTATATTTCAAGAAATGATTT 4510
 QY 584 CATTATTTGAAGTCTTCCCTAGAGGCAATTTCCCTTTTCTGGAAGTTTAGCAAG 643
 DB 4511 CATTATTTGAAGTCTTCCCTAGAGGCAATTTCCCTTTTCTGGAAGTTTAGCAAG 4570
 QY 644 TTAGAGAGATAGTCAATGAAAAAGGAAAGGAGGAGGAGGAGGAGGAGGTTAAAA 703

DB 4571 TTAGAGAGATAGTCAATGAAAAAGGAAAGGAGGAGGAGGAGGAGGAGGTTAAAA 4630
 QY 704 AGTAAGTCTGACAGCTATGAAGCTATGCTTGTGTAATTTTAAAGAGCTGAG 763
 DB 4631 AGTAAGTCTGACAGCTATGAAGCTATGCTTGTGTAATTTTAAAGAGCTGAG 4690
 QY 764 CTGAGTGAAGTGAAGTTTGTCTCAATCAATTTGAGAGAGGATTTTCTGACTGC 823
 DB 4691 CTGAGTGAAGTGAAGTTTGTCTCAATCAATTTGAGAGAGGATTTTCTGACTGC 4750
 QY 824 AATGAGCTGATGTAATTTTATTTTATCACTGAGAAAGCTTGAATGAAATGA 883
 DB 4751 AATGAGCTGATGTAATTTTATTTTATCACTGAGAAAGCTTGAATGAAATGA 4810
 QY 884 ATAAATTTGAGAGTTTCTGTCATATCTGCTGTGATGTCGCAAGAGAGTAAT-A 942
 DB 4811 ATAAATTTGAGAGTTTCTGTCATATCTGCTGTGATGTCGCAAGAGAGTAAT-A 4870
 QY 943 GAAATGTATCTCCAAATCCAAAGCATGAAACCAAGGGGTAGGCAATTTCTATGAG 1002
 DB 4871 GAAATGTATCTCCAAATCCAAAGCATGAAACCAAGGGGTAGGCAATTTCTATGAG 4930
 QY 1003 TTTTGAACAT-GAAGTTGTCATCTTGTATTATGCTGCTCAACTGCTATTAACCTC 1061
 DB 4931 TTTTGAACATGGAAGTTGTCATCTTGTATTATGCTGCTCAACTGCTATTAACCTC 4990
 QY 1062 TCTGGCTTATGCTCTTCAATCTTATGAGACAGCAGTATGAACTGCTTGCACA 1121
 DB 4991 TCTGGCTTATGCTCTTCAATCTTATGAGACAGCAGTATGAACTGCTTGCACA 5050
 QY 1122 AGCTCTTTAGTAAACAATTTAGACGTAATGTTGTGTTAAACAACCTTTCA-CCAA 1180
 DB 5051 AGCTCTTTAGTAAACAATTTAGACGTAATGTTGTGTTAAACAACCTTTCAACCCAA 5110
 QY 1181 TAGGTTTGAAGCAACGAGCAATGACTATTTAAAGAAAGCTTCCAGCATCACT 1240
 DB 5111 TAGGTTTGAAGCAACGAGCAATGACTATTTAAAGAAAGCTTCCAGCATCACT 5170
 QY 1241 ACACATCCCAAAACTAAAAAGATCAACTCTTCAACTGA-GAAAACTCTGCTGTTGA 1299
 DB 5171 ACACATCCCAAAACTAAAAAGATCAACTCTTCAACTGAGAAAGACTCTGCTGTTGA 5230
 QY 1300 ATGG--AACTTACAGCAGAGTCAAGGCAAGGCAACAACAACAACAAC 1356
 DB 5231 ATGGAAACACTTACAGCAGAGTCAAGGCAAGGCAACAACAACAACAAC 5290
 QY 1357 ATTGGAATATTAATTTCACTCACTCACTTTAATTAATTAATTAATTTTCTAGTGA 1416
 DB 5291 ATTGGAATATTAATTTCACTCACTCACTTTAATTAATTAATTAATTTTCTAGTGA 5350
 QY 1417 GAAACTTAAATGAGCTCTTCAACTTATTAATTAATTAATTAATTAATTAATTAAT 1475
 DB 5351 GAAACTTAAATGAGCTCTTCAACTTATTAATTAATTAATTAATTAATTAATTAAT 5410
 QY 1476 ACTTGTCT-CTCACTGAGGTA-TTTTTCCTCCCACTTGCCTGCTCTCTCT 1533
 DB 5411 ACTTGTCTCCCACTGAGGTA-TTTTTCCTCCCACTTGCCTGCTCTCTCTCT 5470
 QY 1534 CC--TCTTCTCTTGGCAAGGAAATTTTAACATATTTGGGTCCTCAATTAAG 1591
 DB 5471 CCATCTGCTCTCTTGGCAAGGAAATTTTAACATATTTGGGTCCTCAATTAAG 5530
 QY 1592 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1649
 DB 5531 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5590
 QY 1650 GCATAGCAAAAACAAAGAAATGCTGA-GAAATTTGCACTGAGACAAGCAATTTGAA 1708
 DB 5591 GCATAGCAAAAACAAAGAAATGCTGAAGAAATTTGCACTGAGACAAGCAATTTGAA 5650
 QY 1709 TAATATTTTCCCAAGTCTTTTATATGATATATGTCAGGATTTGAAGGACTATTT 1768

Db 5651 TAAATATTGGCAAAAGTTCTTTTATGTCATATAGTGTCAAGATTGAGAGCTATT 5710
Qy 1769 TTTTAAATGTCGAAGTCACTGCACTCTTCTGGGAAGACAGCCAGAGAAATGAGTAG 1828
Db 5711 TTTTAAATGTCGAAGTCACTGCACTCTTCTGGGAAGACAGCCAGAGAAATGAGTAG 5770
Qy 1829 AAGTGAAGGTTTAAATTCATTCATTTGTAGACATTTTCCATATATTTTAAATTCAGAA 1888
Db 5771 AAGTGAAGGTTTAAATTCATTCATTTGTAGACATTTTCCATATATTTTAAATTCAGAA 5830
Qy 1889 AAATGTGTTTATCTTAAATTTGTATTCATCTTTAGTACTATAGTACATGCT 1948
Db 5831 AAATGTGTTTATCTTAAATTTGTATTCATCTTTAGTACTATAGTACATGCT 5890
Qy 1949 TCTGATAATTAAGACCAATATGATCTGTAAACCAATCAGACATATTATTATTA 2008
Db 5891 TCTGATAATTAAGACCAATATGATCTGTAAACCAATCAGACATATTATTATTA 5950
Qy 2009 TATATATCTATATTAACAGCCCAAAAAAAAAAGAGAGAGAA 2052
Db 5951 TATATATCTATATTAACAGCCCTCAAAAAAAAAANNNTAAATA 5994

RESULT 3

US-09-439-313-280
; Sequence 280, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1

Qy 1 AAGAGACAGACTATTAATCTCCAGATTAAATTAAGACGATGTCATGTTTATTTGTTA 60
Db 235 AAGAGACAGACTATTAATCTCCAGATTAAATTAAGACGATGTCATGTTTATTTGTTA 294
Qy 61 AAGCAGT 67
Db 295 AAGCAGT 301

RESULT 4
US-09-352-616A-280
; Sequence 280, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi

; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1

RESULT 5

US-09-232-149A-280
; Sequence 280, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1

Qy 1 AAGAGACAGACTATTAATCTCCAGATTAAATTAAGACGATGTCATGTTTATTTGTTA 60
Db 235 AAGAGACAGACTATTAATCTCCAGATTAAATTAAGACGATGTCATGTTTATTTGTTA 294
Qy 61 AAGCAGT 67
Db 295 AAGCAGT 301

RESULT 6
US-09-159-812-280
; Sequence 280, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A

/ CURRENT FILING DATE: 1998-09-23
/ NUMBER OF SEQ ID NOS: 306
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-159-812-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294

QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 7
US-09-636-215-280
/ Sequence 280, Application US/09636215
/ Patent No. 6620922

/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.4271717
/ CURRENT APPLICATION NUMBER: US/09/636,215
/ CURRENT FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-636-215-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294

QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 8
US-09-685-166a-280
/ Sequence 280, Application US/09685166a

/ Patent No. 6630305
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C21
/ CURRENT APPLICATION NUMBER: US/09/685,166a
/ CURRENT FILING DATE: 2000-10-10
/ NUMBER OF SEQ ID NOS: 898
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-685-166a-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294

QY 61 AAGCAGT 67
DB 295 AAGCAGT 301

RESULT 9
US-09-688-489-280
/ Sequence 280, Application US/09688489
/ Patent No. 6664377

/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
/ FILE REFERENCE: 210121.427D2
/ CURRENT APPLICATION NUMBER: US/09/688,489
/ CURRENT FILING DATE: 2000-10-13
/ NUMBER OF SEQ ID NOS: 338
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 280
/ LENGTH: 301
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-688-489-280

Query Match 3.1%; Score 65.4; DB 4; Length 301;
Best Local Similarity 98.5%; Pred. No. 8e-07; 1; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;

QY 1 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 60
DB 235 AAGAGACAGACTATTAACTCCACAGTTAATTAAGACGATGTTCCATGTTTATTGTTA 294

QY 61 AACGACT 67
Db 295 AACGACT 301

RESULT 10

US-09-014-969-14
Sequence 14, Application US/09014969
Patent No. 5965397

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavalie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Valaki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: 32
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 2.6%; Score 54.4; DB 2; Length 2447;
Best Local Similarity 52.2%; Pred. No. 0.00091;
Matches 118; Conservative 1; Mismatches 107; Indels 0; Gaps 0;

QY 1839 TTTATTAATCCATTCTTAAGCATTTATCCCATATATTTAAATGCAAGAAAATTTGCTT 1898
Db 2124 TGTATGATGAGTTTGTGAAAGCTTAATTAATGAGCTGATTAATGATATATATGATCA 2183
QY 1899 TATCTTAGAATTTGTATTCATATCTTATGACTATGCTCATGCTTCTGATTA 1958
Db 2184 CATATCTGATCTGTATATTTGTTTGTACTTAAATGTGCAATTAACCTTTTGGGA 2243
QY 1959 TAAAGCACCAATATGATCTGTATGACCAATGACATCAATATATATTAATATATCTA 2018
Db 2244 GAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2303
QY 2019 TATACAGCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2064
Db 2304 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2349

RESULT 11

US-09-621-976-2813/c
Sequence 2813, Application US/09621976
Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Robert, S.
APPLICANT: Giordano, U.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813

Query Match 2.5%; Score 51.4; DB 4; Length 832;
Best Local Similarity 17.8%; Pred. No. 0.0032;
Matches 82; Conservative 164; Mismatches 215; Indels 0; Gaps 0;

QY 1254 CTAAAGATCACTCTTCCACTGAGAAAGACTCGCTTGAATGGAACCTTACAG 1313
Db 470 CCACAAAGCAAACTTCTCTAAGAAATTAATCACTTGAATGGAACCTTACAG 411
QY 1314 CAGAGCTCAGAGCCAGGCAACCAACAGACACAACTTGAATTAATCTT 1373
Db 410 CAGATTGCTAAGTACAAAGATTGACATAATATATATTTGTATTTGTTTATTTT 351
QY 1374 CACTCAGCTTAAATATCACTTATTTTCTAGAGGAACTCAATACAGC 1433
Db 350 TTYTWTMMWKKKARWYMMKSTYACASRYKRYTGMWYMKMMSTRYCWKC 291
QY 1434 TCTTCAACATTTATATCACTTAAATGAGCTCTTGAAGTTACTTGTCTCACCCTGA 1493
Db 290 CMYGRRCAMYTAAAGGMYANGKMSYMSAMCTMYKKSTYTWKTCATWCY 231
QY 1494 GGTATTTTCTCCCACTTGCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1553
Db 230 YMYTKRMWSKTCWSGSGGMYTSTSTSYMSYMSYMTMCMWGRWSTYMWAMGK 171
QY 1554 GGAATATTTAATATTTGCTCAACTCAATTAATGATATTAATATTAATCAATTAAGC 1613
Db 170 KMWRYATTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 111
QY 1614 ATTTAATCTCTCTTCTAAGAAAATGCAAGGCTTAAGGCTAAGCAACAAAGAAATG 1673
Db 110 TRCAWAAWTKTSYCYWCKWRCMMWMAAAGKTMMAAATTTTAAATTTTAAATTTTAA 51
QY 1674 CTGAGAAATTTGCACTGAGACAGCAAGCAATCTGAATTAATA 1714
Db 50 MMTWMMYMYWRAKMRMMKMSMSMMWMAKMTTAA 10

RESULT 12

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

Query Match 100.0%; Score 2091; DB 2; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGACAGACTTAACTCCACAGTAAATTAAGACGTAATGTCATGTTATTTGTA 60
DB 1 AAGAGACAGACTTAACTCCACAGTAAATTAAGACGTAATGTCATGTTATTTGTA 60
QY 61 AAGCAGTGTAAATAGCCTTCAAGCATGTGAATATCTTCCTCCCGCGCTTTTG 120
DB 61 AAGCAGTGTAAATAGCCTTCAAGCATGTGAATATCTTCCTCCCGCGCTTTTG 120
QY 121 TTTCCTTTCAGTAGACACCTTTTAAATGACAGATTAAGAGGATTCAGTAAGTTG 180
DB 121 TTTCCTTTCAGTAGACACCTTTTAAATGACAGATTAAGAGGATTCAGTAAGTTG 180
QY 181 CTTTCGAATCAATTAAGTCAAAATGTATGAAAATTTTGTGCTTCCTCATACCCG 240
DB 181 CTTTCGAATCAATTAAGTCAAAATGTATGAAAATTTTGTGCTTCCTCATACCCG 240
QY 241 TGTACCAAAATCTCTACTGTATGAATTAATGCTTAAGTAATTCAGTGCAGAGAA 300
DB 241 TGTACTCAAAATCTCTACTGTATGAATTAATGCTTAAGTAATTCAGTGCAGAGAA 300
QY 301 CTGTGTAAATTAATTAATTTTATTTTATCTTTACAAAGCCATGATTTTAT 360
DB 301 CTGTGTAAATTAATTAATTTTATTTTATTTTATCTTTACAAAGCCATGATTTAT 360
QY 361 TGGTGTATGTGTCTCTGACCAAGCATTTCAATAGATGAGCTGTAAATTTTC 420
DB 361 TGGTGTATGTGTCTCTGACCAAGCATTTCAATAGATGAGCTGTAAATTTTC 420
QY 421 CAAAGATATAGACATGCAAAAGTTCAATAAACTGGCCATTAACAAATTAATA 480
DB 421 CAAAGATATAGACATGCAAAAGTTCAATAAACTGGCCATTAACAAATTAATA 480
QY 481 TAACTAATAGCATTCCTTTCTAGTTTTTCCAACTGCTATCCATAACAAATTTG 540
DB 481 TAACTAATAGCATTCCTTTCTAGTTTTTCCAACTGCTATCCATAACAAATTTG 540
QY 541 AAGATCGTGAAGAAAGCTAGTATATTCAGAGAAATGATTTCTATTAAGAACTGTT 600
DB 541 AAGATCGTGAAGAAAGCTAGTATATTCAGAGAAATGATTTCTATTAAGAACTGTT 600
QY 601 TCCCTAGCAGGCAATTTTCCCTTTTCTGGAGTTTAGCAAGTTTAGAGAGAAATGTC 660
DB 601 TCCCTAGCAGGCAATTTTCCCTTTTCTGGAGTTTAGCAAGTTTAGAGAGAAATGTC 660
QY 661 AAGAAAGAAAGGAAAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 661 AAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 ATGAAGCTAATCCCTTTGCTAGAAAATTTTAAGACAGCTCAGCTGTTGAACTGAGT 780
DB 721 ATGAAGCTAATCCCTTTGCTAGAAAATTTTAAGACAGCTCAGCTGTTGAACTGAGT 780
QY 781 TTTGTATCTTCATATTTTGACAGAGATTTTCTGACTTGCAATGAGCTAATGTA 840
DB 781 TTTGTATCTTCATATTTTGACAGAGATTTTCTGACTTGCAATGAGCTAATGTA 840
QY 841 AATTTTATTTTATCTAGTAAAGCCCTGACTAGAAAATGAATTAATTTAGAGGTTT 900
DB 841 AATTTTATTTTATCTAGTAAAGCCCTGACTAGAAAATGAATTAATTTAGAGGTTT 900
QY 901 CCTGTCTATATCTGCTTGCATGTGCGAGAAAGCGAGAAATGTAATCTCCAAC 960
DB 901 CCTGTCTATATCTGCTTGCATGTGCGAGAAAGCGAGAAATGTAATCTCCAAC 960
QY 961 ATCCAAAGCATGAAACCCAGAGGGGTAGGCAATTCATGTAGTTTGGACATGAAGTTG 1020
DB 961 ATCCAAAGCATGAAACCCAGAGGGGTAGGCAATTCATGTAGTTTGGACATGAAGTTG 1020

QY 1021 GTCATCTTGTGTTTANGCTGCTCACTGCTATTAACCTCTGCTTATAGTCTTTC 1080
DB 1021 GTCATCTTGTGTTTANGCTGCTCACTGCTATTAACCTCTGCTTATAGTCTTTC 1080
QY 1081 ATTCTATTAAGACAGACGATATGAAACATCTTGCTTGACAAAGGCTCTTTAGTTAACAT 1140
DB 1081 ATTCTATTAAGACAGACGATATGAAACATCTTGCTTGACAAAGGCTCTTTAGTTAACAT 1140
QY 1141 TTAGCAGCTACTGTGTGTGTTAAACACATTTTCAACCAATAGGTTGAGGCAACGAG 1200
DB 1141 TTAGCAGCTACTGTGTGTGTTAAACACATTTTCAACCAATAGGTTGAGGCAACGAG 1200
QY 1201 AGCAATGACTATTAAGAAAGGCTTCCAGCATCTTACATCCCAAACTAATAAA 1260
DB 1201 AGCAATGACTATTTAAGAAAGGCTTCCAGCATCTTACATCCCAAACTAATAAA 1260
QY 1261 GATCAACTCTTCCACTGAGAAAAGCTCTGCTTGAATGGAACCTTACAGAGAG 1320
DB 1261 GATCAACTCTTCCACTGAGAAAAGCTCTGCTTGAATGGAACCTTACAGAGAG 1320
QY 1321 TCAAGGCCACGCGCAACAAAGCAACAAACAAATTTGGAATTTATCTCACTCA 1380
DB 1321 TCAAGGCCACGCGCAACAAAGCAACAAACAAATTTGGAATTTATCTCACTCA 1380
QY 1381 CGTTTAAATATACATCTTATTAATTTTCTAGTAGAGAACTTACAAATAGCTCTTCA 1440
DB 1381 CGTTTAAATATACATCTTATTAATTTTCTAGTAGAGAACTTACAAATAGCTCTTCA 1440
QY 1441 CATTTATATACATTTTAAATAGGCTCTTGCAAGTTCTGCTACCTGAGGATTT 1500
DB 1441 CATTTATATACATTTTAAATAGGCTCTTGCAAGTTCTGCTACCTGAGGATTT 1500
QY 1501 TTTTCTCCCGACCTTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
DB 1501 TTTTCTCCCGACCTTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
QY 1561 TTTAACAATTTGGGTCCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1620
DB 1561 TTTAACAATTTGGGTCCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1620
QY 1621 TTTCTTTCTAGAAAATGACAGGCTAAGGCTAAGCAAAACAAAGAGAAATGCTAGAA 1680
DB 1621 TTTCTTTCTAGAAAATGACAGGCTAAGGCTAAGCAAAACAAAGAGAAATGCTAGAA 1680
QY 1681 ATTGCGCATGAGACAAAGCAATCTGAATTAATTTTGGCAAAAGTTCTTTTAGTCA 1740
DB 1681 ATTGCGCATGAGACAAAGCAATCTGAATTAATTTTGGCAAAAGTTCTTTTAGTCA 1740
QY 1741 ATAGTCAAGATTTGAAGAGCTATTTTATTTTATGTTGCAACTAGCACTCATCTTC 1800
DB 1741 ATAGTCAAGATTTGAAGAGCTATTTTATTTTATGTTGCAACTAGCACTCATCTTC 1800
QY 1801 GGAAGCAACAGCCAGAGAAATGAAGTGAAGAAAGTTTAAATCAATTTGTAAGCA 1860
DB 1801 GGAAGCAACAGCCAGAGAAATGAAGTGAAGAAAGTTTAAATCAATTTGTAAGCA 1860
QY 1861 TTTATCCATATATTTTAAATTTCAAGAAAATTTGTTATCTTTAGATTTTGTATTA 1920
DB 1861 TTTATCCATATATTTTAAATTTCAAGAAAATTTGTTATCTTTAGATTTTGTATTA 1920
QY 1921 ATACTTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 ATACTTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 TAAACCAATCAACATATTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTA 2040
DB 1981 TAAACCAATCAACATATTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTA 2040
QY 2041 AGAAG 2091
DB 2041 AGAAG 2091

RESULT 2
AA298079
ID AA298079 standard; cDNA, 3674 BP.
XX
AC AA298079;
XX
DT 09-MAY-2000 (first entry)
XX
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:73.
XX
KW Human, secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiinflammatory; nootropic; neuroprotective; antiallergic; cancer;
KW tumour; neurodegenerative disorder; developmental abnormality; allergy;
KW foetal deficiency; blood disorder; immune system disorder; arthritis;
KW autoimmune disease; hepatic disease; renal disease; inflammation;
KW Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;
KW infection; AIDS; spinal cord injury; transplant rejection; diabetes;
KW asthma; sepsis; acne; psoriasis; cardiovascular disorder;
KW reproductive disorder; gastrointestinal disorder; respiratory disorder;
KW metabolic disorder; food additive; preservative; ss.
XX
OS Homo sapiens.
XX
PN WO200004140-A1.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015849.
XX
PR 15-JUL-1998; 98US-0092921P.
PR 15-JUL-1998; 98US-0092922P.
PR 15-JUL-1998; 98US-0092956P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;
PI Lafleur DW, Ehner R, Olsen HS, Brewer LA, Florence KA, Young PE;
PI Mucenki M, Endress GA, Soppet DR;
XX
DR WP1: 2000-161128/14.
DR P-PSDB; AAY87126.
XX
PT New isolated human genes, useful for diagnosis and treatment of, e.g.
PT cancers, neurological or blood disorders.
XX
PS Claim 1; Page 348-349; 494pp; English.
XX
SS The polynucleotide sequences given in AA298017 to AA298108 encode the
CC human secreted proteins given in AAY87064 to AAY87223. Human secreted
CC protein can have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic;
CC immunosuppressive; antiinflammatory; nootropic; neuroprotective; and
CC antiallergic. The polynucleotides and their corresponding secreted
CC polypeptides are useful for preventing, treating or ameliorating medical
CC conditions, e.g. by protein or gene therapy. Also pathological conditions
CC can be diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new
CC polynucleotides. Human secreted proteins and their polynucleotides can
CC be used for developing products for the diagnosis or treatment of cancer,
CC tumour, neurodegenerative disorders, developmental abnormalities and
CC foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's disease, behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AA298008 to AA298016 and AAY87063 are
CC sequence used in the exemplification of the present invention
XX
SQ Sequence 3674 BP; 1221 A; 670 C; 624 G; 1159 T; 0 U; 0 Other;

Query Match 95.8%; Score 2003.8; DB 3; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2034; Conservative 0; Mismatches 7; Indels 16; Gaps 1;
QY 1 AAGAGACGACCTTAACTCCACAGTTAATTAAGACGATGTCACGTTATTTGTTA 60
DB 1617 AAGAGACGACCTTAACTCCACAGTTAATTAAGACGATGTCACGTTATTTGTTA 1676
QY 61 AAGCAGTGTGAATAGCTTCAAGCATGTGAATTAATCTTCCATCTTCCCGC----- 111
DB 1677 AAGCAGTGTGAATAGCTTCAAGCATGTGAATTAATCTTCCATCTTCCCGCAGCATATC 1736
QY 112 -----CGCTTTTGTGTTCTTTCAGGTAGACCTTTTAAATGACAACTAATGAG 164
DB 1737 ACACACACCTTTTGTGTTCTTTCAGGTAGACCTTTTAAATGACAACTAATGAG 1796
QY 165 CATTTCAGTACTTGTGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 224
DB 1797 CATTTCAGTACTTGTGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1856
QY 225 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAATTATGCTTTAAGTAGAT 284
DB 1857 TACTCTCCATACCCCGTGTACTCAATCTCTACTGTATGAATTATGCTTTAAGTAGAT 1916
QY 285 TCAGTGCCCAAGAGAACTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 344
DB 1917 TCAGTGCCCAAGAGAACTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1976
QY 345 AAGCATGATTTTATTTGTTGATGTGTCTGTGACACAGCCATTTCAATGATGATGCA 404
DB 1977 AAGCATGATTTTATTTGTTGATGTGTCTGTGACACAGCCATTTCAATGATGATGCA 2036
QY 405 GCTGTTAATTAATTTTCCAAAGTAAATGACATGCAAAAGTTCAATTAATTAATTAATTAAT 464
DB 2037 GCTGTTAATTAATTTTCCAAAGTAAATGACATGCAAAAGTTCAATTAATTAATTAATTAAT 2096
QY 465 TTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
DB 2097 TTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2156
QY 525 TCCATTAACAAATTTGAGATGTTGAAAAAGCTATGTTATTTGAGAAATGATTTTTC 584
DB 2157 TCCATTAACAAATTTGAGATGTTGAAAAAGCTATGTTATTTGAGAAATGATTTTTC 2216
QY 585 ATTATTAACAACTGTTCTCCCTAGCAGGCAATTTTCCCTTTTCTGGAGTTTACCAAGT 644
DB 2217 ATTATTAACAACTGTTCTCCCTAGCAGGCAATTTTCCCTTTTCTGGAGTTTACCAAGT 2276
QY 645 TTAGAGAGAAATGATGATGAAAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
DB 2277 TTAGAGAGAAATGATGATGAAAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2336
QY 705 GTTAAAGCTCAACCTATGAATGATGAAAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAG 764
DB 2337 GTTAAAGCTCAACCTATGAATGATGAAAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAG 2396
QY 765 TTGTTGAACCTGAGTTTGTGATCTTCCATATTTGACAGAAAGGATTTTGTGACTTGA 824
DB 2397 TTGTTGAACCTGAGTTTGTGATCTTCCATATTTGACAGAAAGGATTTTGTGACTTGA 2456
QY 825 ATGACGCTGATGATTAATTTATTTATTCATCCATGAAAGGCTGACATGAAATGAA 884
DB 2457 ATGACGCTGATGATTAATTTATTTATTCATCCATGAAAGGCTGACATGAAATGAA 2516
QY 885 TAAATATTAAGGTTTCTGTCATATCTGAGTTGATGTCAGAAAGCAGAGATGAA 944
DB 2517 TAAATATTAAGGTTTCTGTCATATCTGAGTTGATGTCAGAAAGCAGAGATGAA 2576
QY 945 AATATTAATCTCAACATCCAGATCCAGAAAGGAGTGGCAATCTTATGAGGTT 1004
DB 2577 AATATTAATCTCAACATCCAGATCCAGAAAGGAGTGGCAATCTTATGAGGTT 2636
QY 1005 TTGACATGAAGTTTGTGATCTTGTATGCTGCTCAACTGATTAATTAATCTCTCT 1064

Db 2637 TTGGAAATGAAGTTGGTGCATCTTGTTTATGCTGGCTCAACGATGATTAACCTCTCT
 QY 1065 GGGTTATAGTCTCTTCATTCATTTAGACAAGACGATGCAACATCTGGTGGACAAG 1124
 Db 2697 GGGTTATAGTCTCTTCATTCATTTAGACAAGACGATGCAACATCTGGTGGACAAG 2756
 QY 1125 CTCTTAGTTAAACAATTTAGACCTACTGTTTGTGTTAAACACATTTTCCACCAATAG 1184
 Db 2757 CTCTTAGTTAAACAATTTAGACCTACTGTTTGTGTTAAACACATTTTCCACCAATAG 2816
 QY 1185 TTCTGAGGCAACGAGAGCAATGACTATTTAAAGAAAGCTTTCCAGCATCACTTAC 1244
 Db 2817 TTCTGAGGCAACGAGAGCAATGACTATTTAAAGAAAGCTTTCCAGCATCACTTAC 2876
 QY 1245 ATCCCAAAACTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCTTTGAATGA 1304
 Db 2877 ATCCCAAAACTAAAGATCACTCTTCCACTGAGAAAAGACTCTGGCTTTGAATGA 2936
 QY 1305 AACTACAGCAGAGTCAACAGGCCACAGGCAACAAACAACAACAAACATTTGGA 1364
 Db 2937 AACTACAGCAGAGTCAACAGGCCACAGGCAACAAACAACAACAAACATTTGGA 2996
 QY 1365 TATTATTCTCACTCACTGTTTAAATAATACATCTTATTTTCTAGTAGAGAAACTAC 1424
 Db 2997 TATTATTCTCACTCACTGTTTAAATAATACATCTTATTTTCTAGTAGAGAAACTAC 3056
 QY 1425 AATACAGCCTCTCAACATTTATATACGTTTAAATAGCCTCTGCAAGTCTTCT 1484
 Db 3057 AATACAGCCTCTCAACATTTATATACGTTTAAATAGCCTCTGCAAGTCTTCT 3116
 QY 1485 CTCACCTGAGATATTTTCTCTCCACCTGCTGCTGCTCTCTCTCTCTCTCTCT 1544
 Db 3117 CTCACCTGAGATATTTTCTCTCCACCTGCTGCTGCTGCTCTCTCTCTCTCTCT 3176
 QY 1545 TTGCAAGAGGAATTTTAACTATTTGGGTGCAACTCAATATATATATATATATAT 1604
 Db 3177 TTGCAAGAGGAATTTTAACTATTTGGGTGCAACTCAATATATATATATATATAT 3236
 QY 1605 ATTAAAGCATTTTACTCTCTCTCTAGAAAATGCAAGGCTAAGCATAGACAACA 1664
 Db 3237 ATTAAAGCATTTTACTCTCTCTCTAGAAAATGCAAGGCTAAGCATAGACAACA 3296
 QY 1665 AGGAAATGCTGGAATTTGCACTGAGACAAGAAATCTAAATTAATTTGGCAAA 1724
 Db 3297 AGGAAATGCTGGAATTTGCACTGAGACAAGAAATCTAAATTAATTTGGCAAA 3356
 QY 1725 GTTCTTTTATGTCATATAGTGTGAGATTTTGAAGAGCTATTTTATATGTTGCA 1784
 Db 3357 GTTCTTTTATGTCATATAGTGTGAGATTTTGAAGAGCTATTTTATATGTTGCA 3416
 QY 1785 CTGGAACCTCATTTTGGGAAGACACGCGAGGAATGAAGTGAAGTGAAGTGTATA 1844
 Db 3417 CTGGAACCTCATTTTGGGAAGACACGCGAGGAATGAAGTGAAGTGAAGTGTATA 3476
 QY 1845 AATCCATTTGTAAGATTTATCCCATATATTTTAAATCAAGAAAATGTGTTATCTT 1904
 Db 3477 AATCCATTTGTAAGATTTATCCCATATATTTTAAATCAAGAAAATGTGTTATCTT 3536
 QY 1905 TAGAATTTGTATCAATACTTATATGTAATGTAAGTCAATGCTTGTGATTAATAG 1964
 Db 3537 TAGAATTTGTATCAATACTTATATGTAATGTAAGTCAATGCTTGTGATTAATAG 3596
 QY 1965 ACAAAATATGATCTGTAACCAACATCAACATATATATTAATATATATATATATAC 2024
 Db 3597 ACAAAATATGATCTGTAACCAACATCAACATATATATTAATATATATATATATAC 3656
 QY 2025 AGCCAAAAA 2041
 Db 3657 AAAAAA 3673

RESULT 3

AAD11692
 ID AAD11692 standard; cDNA; 3674 BP.
 AC AAD11692;
 XX 24-SEP-2001 (first entry)
 DE Human secreted protein-encoding gene 63 cDNA clone HUVB077, SHQ ID NO:73.
 XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; hematopoietic disorder;
 KW immune system disease; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KW cell culture; Chemotaxis; vulnirary; binding partner identification;
 KW gene therapy; ss.
 KW Homo sapiens.
 OS
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 55..198
 FT /*tag= a
 FT /product= "Human secreted protein precursor"
 FT 55..135
 FT /*tag= b
 FT mat_peptide
 FT 135..195
 FT /*tag= c
 FT /product= "Mature human secreted protein"
 FT
 FN WO200151504-A1.
 PN 19-JUL-2001.
 PD 12-JAN-2001; 2001MO-US000911.
 PE 13-JAN-2000; 2000US-00482273.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Komatsu-Lie GA, Duan DR, Rosen CA, Moore PA, Shi Y;
 PI Laflair DW, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;
 PI Endress GA, Muscenski M, Edner R;
 XX WPI; 2001-425865/45.
 DR P-PSDB; AAE06103.
 DR
 XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 1; Page 715-716; 864pp; English.
 CC AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
 CC protein genes, and AAE06041-AAE06132 represent the proteins they encode.
 CC AAE06133-AAE06205 represent human secreted protein fragments. The
 CC secreted proteins and their genes are useful for preventing, treating or
 CC ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 71 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell

Dd	3537 TAGAATTTCGATTAACACTTAACTTAAGTCACTAGTACCACTCGCTTGAGATAAATAAGC	3596
Oy	1965 ACCAAATATGTATCTGTGAACCAATCACCATATTAATTAAATATATCTATATTAAC	2022
Dd	3597 ACCAAATATGTATCTGTGAACCAATCACCATATTAATTAAATATATCTATATTAAC	3656
Oy	2025 AGCCAAAAAAAAAAAAA 2041 3657 AAAAAAAAAAAAAAAAAA 3673	
Dd		
RESULT 4		
ABK69788		
ID	ABK69788 standard; cDNA; 3674 BP.	
XX	ABK69788;	
XX		
DT	15-JUL-2002 (first entry)	
DE		
Human secreted protein gene 63.		
XX		
Human; ss; gene; secreted protein; gene therapy; immunosuppressive;		
KW	antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;	
KW	vaccitropic; cerebroprotective; nootropic; neuroprotective; antibacterial;	
KW	vinciclovir; fungicide; ophthalmological; autoimmune disease; neoplasm;	
KW	rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;	
KW	cardiovascular disorder; cerebrovascular disorder; cerebral ischemia;	
KW	angiogenesis; nervous system disorder; Alzheimer's disease; infection;	
KW	ocular disorder; corneal infection; wound healing; skin aging;	
KM	epithelial cell proliferation; food additive.	
OS	Homo sapiens.	
PN	WO200226931-A2.	
XX		
PT	04-APR-2002.	
XX		
24-SEP-2001; 2001WO-US029871.		
XX		
25-SEP-2000; 2000US-0234925P.		
PR	12-JAN-2001; 2001MO-US000911.	
XX		
(HUMAN-) HUMAN GENOME SCI INC.		
PI	Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y,	
PI	Lafleur DW, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;	
PI	Andress GA, Mucenski M, Edner R;	
XX		
WP1, 2002-362489/39.		
DR	P-PSTDB; ABG33925.	
XX		
Novel 71 isolated secreted polypeptides and polynucleotides encoding the		
polypeptides, useful for treating Huntington's disease, sepsis,		
meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,		
asthma.		
Claim 1; Page 1197-1198; 1478pp; English.		
The invention relates to an isolated nucleic acid molecule (or its		
fragment, homologous complement or allelic variant) encoding a human		
secreted protein (and its fragment, domain, epitope, variant, secreted		
form and species variant). Also included are a recombinant vector		
comprising the nucleic acid, a recombinant host cell comprising the		
vector, an antibody against the secreted protein, a recombinant host cell		
that expresses the secreted protein and a method of identifying a binding		
partner of the secreted protein. The nucleic acid and protein are used to		
prevent, diagnose, treat or ameliorate a medical condition in e.g.		
humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for		
example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative		
disorders e.g. neoplasms of the breast or liver, cardiovascular disorders		
e.g. cardiac arrest, cerebrovascular disorder e.g. cerebral ischaemia,		
angiogenesis, nervous system disorders e.g. Alzheimer's disease,		

	infections caused by bacteria, viruses and fungi and ocular disorders					
Cc	e.g. corneal infection. Many other diseases and disorders are listed in					
Cc	the specification. The polypeptides can also be used to aid wound healing					
Cc	an epithelial cells before proliferation, to prevent skin aging due to sunburn' of					
Cc	to maintain organs before transplantation, for supporting cell culture of					
Cc	primary tissues, to regenerate tissues and in chemotaxis. The					
Cc	polypeptides can also be used as a food additive or preservative to					
Cc	increase or decrease storage capabilities. The present sequence encodes a					
Cc	novel human secreted protein of the invention					
XX						
SQ	Sequence 3674 BP; 1221 A; 670 C; 624 G; 1159 T; 0 U; 0 Other;					
	Query Match	95.8%;	Score 2003.8;	DB 6;	Length 3674;	
	Best Local Similarity	98.3%;	Pred. No. 0/			
	Matches 2034;	Conservative	0;	Mismatches	7;	Indels 16;
					Gaps	1;
QY	1	AAGGACAGCACTAATTAACTCCACAGTAATTTAAGAGCGTATGTTCAGTGTATTTTGTA	60			
Db	1617	AAGGACAGCACTAATTAACTCCACAGTAATTTAAGAGCGTATGTTCAGTGTATTTTGTA	1676			
QY	61	AAGGAGTGTGAATAGCCTTCAAGCATGTGAATACTTCCACTCTCCCGC-----	111			
Db	1677	AAGGAGTGTGAATAGCCTTCAAGCATGTGAATACTTCCACTCTCCCGCACACAATAC	1736			
QY	112	-----CGCTTTTGTTCCTTTNAGGTGAGCACCTTTTAAAAGGAGAATACTAGG	164			
Db	1737	ACACACACACTTTTGTTCCTTTNAGGTGAGCACCTTTTAAAAGGAGAATACTAGG	1796			
QY	165	CATTTCAGTACTTGGCTTCCAATTCATAAAGTCAATGTATGAAACATTTGTGCC	224			
Db	1797	CATTTCAGTACTTGGCTTCCAATTCATAAAGTCAATGTATGAAACATTTGTGCC	1856			
QY	225	TACTCTCATACCCCGGTATCTCAAATTTCTTACTGTATGAAATATGCTTTAAGTAGAT	284			
Db	1857	TACTCTCATACCCCGGTATCTCAAATTTCTTACTGTATGAAATATGCTTTAAGTAGAT	1916			
QY	285	TCAGTGCACAAAGAGAACCTGTGGAATTAATTATTTTTTTTTTATCTCTTACAA	344			
Db	1917	TCAGTGCACAAAGAGAACCTGTGGAATTAATTATTTTTTTTTTATCTCTTACAA	1976			
QY	345	AGCCATGATTTTATTTGGTGTGATGTGTCTGTACACAGCCATTTCAATAGATGGA	404			
Db	1977	AGCCATGATTTTATTTGGTGTGATGTGTCTGTACACAGCCATTTCAATAGATGGA	2036			
QY	405	GCTGTTATTTTTCCTCCAAAGATPATGACATGGAAAAAGTTCCATTAACCTGGSCCA	464			
Db	2037	GCTGTTATTTTTCCTCCAAAGATPATGACATGGAAAAAGTTCCATTAACCTGGSCCA	2096			
QY	465	TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	524			
Db	2097	TTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2156			
QY	525	TCCATTAACAAATTTGAGATTCGTTGAAAAAGCTGTAATTTTACAGAAATGATTTTC	584			
Db	2157	TCCATTAACAAATTTGAGATTCGTTGAAAAAGCTGTAATTTTACAGAAATGATTTTC	2216			
QY	585	ATTATTTGAAACGTCTCTCCCTAGCAGGCCATTTTCCCTTTTTCCTGGAGTTTACCAAT	644			
Db	2217	ATTATTTGAAACGTCTCTCCCTAGCAGGCCATTTTCCCTTTTTCCTGGAGTTTACCAAT	2276			
QY	645	TTAGAGAGAAATPAGTATGAAAAAGAAAGGAGAAAGGAGAGAAAGAGTTAAAAA	704			
Db	2277	TTAGAGAGAGAAATPAGTATGAAAAAGAAAGGAGAAAGGAGAGAAAGAGTTAAAAA	2336			
QY	705	GTPAAGTGCACAGCCTATGAAAGTATCCCTTGTCTAGAAAAATTTTAAAGCAGCTCAGC	764			
Db	2337	GTPAAGTGCACAGCCTATGAAAGTATCCCTTGTCTAGAAAAATTTTAAAGCAGCTCAGC	2396			
QY	765	TTGGTTGAAACTGAGTTTGTTCATCTTCCATATTTTGACGAAAGGTAATTTTCTGACTTGA	824			
Db	2397	TTGGTTGAAACTGAGTTTGTTCATCTTCCATATTTTGACGAAAGGTAATTTTCTGACTTGA	2456			
QY	825	ATGCAAGCTAGATGTAATTTTATTTTATTCATCTCAGAAAGCCTGACTAGAAAAATGAA	884			


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Db      2457 ATGAGCTAGATGAAATTTTATTTATATCATCTGAAAGCCCTTGACTGAAATTAAG 2516
Qy      885 TAAATATTTGAGGGTTTCTGTCATATCTGCTTGACATGTGCAGAAAGAGAAATAG 944
Db      2517 TAAATATTTGAGGGTTTCTGTCATATCTGCTTGACATGTGCAGAAAGAGAAATAG 2576
Qy      945 AAATGATATCTCCAACTCCAAAGATGAAACCCAGGGGTAGGCAATTTATGTAGT 1004
Db      2577 AAATGATATCTCCAACTCCAAAGATGAAACCCAGGGGTAGGCAATTTATGTAGT 2636
Qy      1005 TTGACATGAGTTGGTGCATCTGGTTATGTGGCTCACTGATTAATTAACCTCTCT 1064
Db      2637 TTGACATGAGTTGGTGCATCTGGTTATGTGGCTCACTGATTAATTAACCTCTCT 2696
Qy      1065 GGGTTATAGTCTCTTCACTTATTTAGCAAGACAGTTCGAAACATCTGCTGGCAAG 1124
Db      2697 GGGTTATAGTCTCTTCACTTATTTAGCAAGACAGTTCGAAACATCTGCTGGCAAG 2756
Qy      1125 CTCTTTAGTTAACAATTTAGAGCTAGCTGTTGTGTAACACACTTTGACCAAAATAG 1184
Db      2757 CTCTTTAGTTAACAATTTAGAGCTAGCTGTTGTGTAACACACTTTGACCAAAATAG 2816
Qy      1185 TTCTGAGCAAAACGAGAGCAATGACTTTTAAAGAAAGCTTTCCAGCATCACTTAAC 1244
Db      2817 TTCTGAGCAAAACGAGAGCAATGACTTTTAAAGAAAGCTTTCCAGCATCACTTAAC 2876
Qy      1245 ATCCCAAACTTAAAGATCACTCTTCCAGTGAAGAAAGACTCTGGCTTTGATGGA 1304
Db      2877 ATCCCAAACTTAAAGATCACTCTTCCAGTGAAGAAAGACTCTGGCTTTGATGGA 2936
Qy      1305 AACTTACAGCAGAGTCAAGGCGCAGGCAACAGCAACAAACAACTTTGGA 1364
Db      2937 AACTTACAGCAGAGTCAAGGCGCAGGCAACAGCAACAAACAACTTTGGA 2996
Qy      1365 TATATTTCTCACTCACTTTTATTAATACATCTTATTTTCTAGTAGAAGAACTAC 1424
Db      2997 TATATTTCTCACTCACTTTTATTAATACATCTTATTTTCTAGTAGAAGAACTAC 3056
Qy      1425 AATCAGGCTCTTCAACATTTATATATAGTTAAAGCTCTTCAAGTACTGTCT 1484
Db      3057 AATCAGGCTCTTCAACATTTATATATAGTTAAAGCTCTTCAAGTACTGTCT 3116
Qy      1485 CTCACCTGAGGATTTTTTCTCCCACTGCTGCTGCTCTCTCTCTCTCTCTCTCT 1544
Db      3117 CTCACCTGAGGATTTTTTCTCCCACTGCTGCTGCTCTCTCTCTCTCTCTCTCT 3176
Qy      1545 TTGCAAGAGGAATTTATATATATGAGTCCCACTCAATTAATTAATTAATTAAT 1604
Db      3177 TTGCAAGAGGAATTTATATATATGAGTCCCACTCAATTAATTAATTAATTAAT 3236
Qy      1605 ATTAAGAGCATTTAATCTCTTCTAGAAAATGACAGGCTTAAGGATAGACAAACAA 1664
Db      3237 ATTAAGAGCATTTAATCTCTTCTAGAAAATGACAGGCTTAAGGATAGACAAACAA 3296
Qy      1665 AGAAGAAATGCGAAGAAATTTGCGCATGAGAGCAAGCAATCGAATAAATTTTGGCCAAA 1724
Db      3297 AGAAGAAATGCGAAGAAATTTGCGCATGAGAGCAAGCAATCGAATAAATTTTGGCCAAA 3356
Qy      1725 GTTCTTTTATATGATATAGTGTGAGATTTGAAGAGCTAATTTTTTTTAAATGTTGCA 1784
Db      3357 GTTCTTTTATATGATATAGTGTGAGATTTGAAGAGCTAATTTTTTTTAAATGTTGCA 3416
Qy      1785 CTAGCAATCTATCTTCCGAACACAGCAGAGAAATGAAGTAAAGTAAAGTTATATA 1844
Db      3417 CTAGCAATCTATCTTCCGAACACAGCAGAGAAATGAAGTAAAGTAAAGTTATATA 3476
Qy      1845 AATCATTTGTAAGATTTATCCATATATTTTAAATTCAGAAATTTGTGTTATCTT 1904
Db      3477 AATCATTTGTAAGATTTATCCATATATTTTAAATTCAGAAATTTGTGTTATCTT 3536
Qy      1905 TAGAATTTTGTATCAATCTTATATGATGACTAGCTTCTGATTAATTAAGC 1964

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Db      3537 TAGAATTTTGTATCAATCTTATATGATGACTAGCTTCTGATTAATTAAGC 3596
Qy      1965 ACCAAATATGATCTGTAAACAATCAACAATATTAATTAATTAATTAATTAAC 2024
Db      3597 ACCAAATATGATCTGTAAACAATCAACAATATTAATTAATTAATTAATTAAC 3656
Qy      2025 AGCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2041
Db      3657 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3673

RESULT 5
ABK69943
ID ABK69943 standard; DNA; 10427 BP.
XX
XX
AC ABK69943;
XX
XX
DT 15-JUL-2002 (first entry)
XX
XX
DE Human secreted protein gene 69 genomic DNA fragment #2.
XX
XX
KW Human; ds; secreted protein; gene therapy; immunosuppressive;
KW antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
KW vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial;
KW vincidine; fungicide; ophthalmological; autoimmune disease; neoplasm;
KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; skin aging;
KW epithelial cell proliferation; food additive.
XX
XX
OS Homo sapiens.
XX
XX
PN MO200226931-A2.
XX
XX
PD 04-APR-2002.
XX
XX
PF 24-SEP-2001; 2001MO-US029871.
XX
XX
PR 25-SEP-2000; 2000US-0234925P.
XX
XX
PI 12-JAN-2001; 2001MO-US000911.
XX
XX
PI (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Ruben SM, Komatsculis G, Duan DR, Rosen CA, Moore PA, Shi Y;
PI Lafleur DW, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;
PI Andrews GA, Mucenski M, Ebner R;
XX
XX
DR WPI; 2002-362489/39.
XX
XX
PT Novel 71 isolated secreted polypeptides and polynucleotides encoding the
PT polypeptides, useful for treating Huntington's disease, sepsis,
PT meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,
PT asthma.
XX
XX
PS Example 2; Page 1452-1455; 1478pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid molecule (or its
CC fragment, homologue complement or allelic variant) encoding a human
CC secreted protein (and its fragment, domain, epitope, variant, secreted
CC form and species variant). Also included are a recombinant vector
CC comprising the nucleic acid, a recombinant host cell comprising the
CC vector, an antibody against the secreted protein, a recombinant host cell
CC that expresses the secreted protein and a method of identifying a binding
CC partner of the secreted protein. The nucleic acid and protein are used to
CC prevent, diagnose, treat or ameliorate a medical condition in e.g.
CC humans, mice, rabbits, goats, cats, dogs, chickens or sheep for
CC example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. Many other diseases and disorders are listed in

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the specification. The polypeptides can also be used to aid wound healing of an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in cosmetics. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a ds DNA fragment of the gene for a novel human secreted protein of the invention

Sequence 10427 BP; 3337 A; 1995 C; 1829 G; 3266 T; 0 U; 0 Other;

Query Match	95.7%;	Score 2000.4;	DB 6;	Length 10427;
Best Total Similarity	99.3%;	Score No. 0;		

Matches 2027; Conservative 0; Mismatches 1; Indels 16; Gaps 1;

OY		L	AAGGACACACATATACTTCCACAGTAATAAAGAGAGATATTCAGATGTTATTGGTGA	86
Db	8383	AAGGACACAGCATATTAATCACCAGATTATTAAGAGAGATATTCAGATGTTATTGGTGA	8442	
OY	61	AAGAGGTGTAATAGCCTTCAGAAGATGGAATATCTCCATCTTCCCGC-----	111	
Db	8443	AAGCAGTGATATAGCCTTCAGAAGATGGAATATCTCCATCTTCCCGCACAACATAC	8502	
OY	112	-----CGCTTTTGTTTTCTTTCAAGTAGACACCTTTAAATGCGAAGTAACGTAGG	164	
Db	8503	ACACACACACTTTTGTTTTCTTTCAAGTAGACACCTTTAAATGCGAAGTAACGTAGG	8562	
OY	165	CATTTCAGTACTTGTGCTTCAAATGCATAAAGTCAATGATGAGAAAATTGTGTGCC	224	
Db	8563	CATTTCAGTACTTGTGCTTCAAATGCATAAAGTCAATGATGAGAAAATTGTGTGCC	8622	
OY	225	TACTTCCATACCCCGTACTCAAACTCTACGTATGAAATATAGCTTAAGTAGAT	284	
Db	8623	TACTTCCATACCCCGTACTCAAACTCTACGTATGAAATATAGCTTAAGTAGAT	8682	
OY	285	TCAGTCCAGAGAGAACTGTGAAATTAATTTTAAATTTTTTTTAACTCTTACA	344	
Db	8683	TCAGTCCAGAGAGAACTGTGAAATTAATTTTAAATTTTTTTTAACTCTTACA	8742	
OY	345	AGCCATGATTTTATTTGGTGAATGTGTCCTGTGACACAGCCATTCAATAGATAGA	404	
Db	8743	AGCCATGATTTTATTTGGTGAATGTGTCCTGTGACACAGCCATTCAATAGATAGA	8802	
OY	405	GCTGTTAATTATTTCCAAAGAGTATAGACATGCAAAAGTTTCATTAATAACTGTGGCCA	464	
Db	8803	GCTGTTAATTATTTCCAAAGAGTATAGACATGCAAAAGTTTCATTAATAACTGTGGCCA	8862	
OY	465	TTAACAAATTAATTATTAACCTAATAGCATTCCTCTAGGTTTTCGCAACCTGCCTA	524	
Db	8863	TTAACAAATTAATTATTAACCTAATAGCATTCCTCTAGGTTTTCGCAACCTGCCTA	8922	
OY	525	TCCAATACAAATTTGAGAACTGTTGAAAAAGCTAGTTATTTCCAGAAATGATTTTC	584	
Db	8923	TCCAATACAAATTTGAGAACTGTTGAAAAAGCTAGTTATTTCCAGAAATGATTTTC	8982	
OY	585	ATTATGGAACGTGCTCCCTGACAGGCGCATTTTCCCTTTCCGGAGTTTAGCAAGT	644	
Db	8983	ATTATGGAACGTGCTCCCTGACAGGCGCATTTTCCCTTTCCGGAGTTTAGCAAGT	9042	
OY	645	TTAGAGAGAAATAGTCATGAAAAGAAAGGAAAGAAAGGAGAGAAAGGTTAAAAA	704	
Db	9043	TTAGAGAGAAATAGTCATGAAAAGAAAGGAAAGAAAGGAGAGAAAGGTTAAAAA	9102	
OY	705	GTAAGTGCTAGACCTATGAACGTATCCCTTGTCTAGAAATATTTAAGACAGCTCAGC	764	
Db	9103	GTAAGTGCTAGACCTATGAACGTATCCCTTGTCTAGAAATATTTAAGACAGCTCAGC	9162	
OY	765	TTGTTGAACTGAGTTTGTTCATCTTCATATTTGACAGAAAGTAATTTCTGACTTGCA	824	
Db	9163	TTGTTGAACTGAGTTTGTTCATCTTCATATTTGACAGAAAGTAATTTCTGACTTGCA	9222	
OY	825	ATGCAGCTGATGTAAAAATTTATTTTATCATCTTAGAAGACCTGACTAGAAAAATGAA	884	

Db	9223	ATGCAAGTAGATGTAATAATTTATTTATTCATCTGAGAAAGGCTTGACTAGAAAATATGAA	9282
Qy	885	TAATAATATGAGGGTTTCCTGTCATPATCGGTGTCATCTGCGCAGAAAGCAGAGAAATGGA	944
Db	9283	TAATATATGAGGGTTTCCTGTCATPATCGGTGTCATCTGCGCAGAAAGCAGAGAAATGGA	9342
Qy	945	AAATGTAAATCCAGCATCCAGCATCGAAACCCAGGGGTAGCGAATTCATATGTAGGTT	1004
Db	9343	AAATGTAAATCCAGCATCCAGCATCGAAACCCAGGGGTAGCGAATTCATATGTAGGTT	9402
Qy	1005	TTGGACATGAAGTTTGGTGATCTTGGTTTATGCTGGGCTCAACCTGCTATTAACCTCTCT	1064
Db	9403	TTGGACATGAAGTTTGGTGATCTTGGTTTATGCTGGGCTCAACCTGCTATTAACCTCTCT	9462
Qy	1065	GGCTTATAGCTCTTTCATCTATATAGACAAAGCAGATCGAAACCTTCTTCGACAAAG	1124
Db	9463	GGCTTATAGCTCTTTCATCTATATAGACAAAGCAGATCGAAACCTTCTTCGACAAAG	9522
Qy	1125	CTCTTATAGTTAACATTTTAGACGCTATCTGTGTGTAAACAACCTTTTCAACMAATAGG	1184
Db	9523	CTCTTATAGTTAACATTTTAGACGCTATCTGTGTGTAAACAACCTTTTCAACMAATAGG	9582
Qy	1185	TTCTGAGGCAAACGAGAGCAATGACATTTAAGAAAGGCTTCCAGACATCACTTAAC	1244
Db	9583	TTCTGAGGCAAACGAGAGCAATGACATTTAAGAAAGGCTTCCAGACATCACTTAAC	9642
Qy	1245	ATCCCAAACTAAAAAATCAACTCTCTCCACATGAGAAAGACCTCTGCTTTGAAATGGA	1304
Db	9643	ATCCCAAACTAAAAAATCAACTCTCTCCACATGAGAAAGACCTCTGCTTTGAAATGGA	9702
Qy	1305	AACCTACAGCAGAGAGTCAAGGCCACGGCCACACAGACAAACAACAAATTTGGAA	1364
Db	9703	AACCTACAGCAGAGAGTCAAGGCCACGGCCACACAGACAAACAACAAATTTGGAA	9762
Qy	1365	TATATATCTACATCGAGTTTATATATATACATCTTATTTTCTAGTAGAAACTAC	1424
Db	9763	TATATATCTACATCGAGTTTATATATATACATCTTATTTTCTAGTAGAAACTAC	9822
Qy	1425	AAATCAGCCCTCTTCAACATTTATATACAGTTTATAGCCCTCTTGCAGTACTTGTTCT	1484
Db	9823	AAATCAGCCCTCTTCAACATTTATATACAGTTTATATAGCCCTCTTGCAAGTACTTGTTCT	9882
Qy	1485	CTCACCAGAGATTTTTTTCGCCGCCACCTGCCCCCTGCTCCTCCCTCCCTCTCC	1544
Db	9883	CTCACCAGAGATTTTTTTCGCCGCCACCTGCCCCCTGCTCCTCCCTCCCTCTCC	9942
Qy	1545	TTTGCAAGAGAAATATTTAACAATATTTGGGTCCAACTTCAATATATATATATATAC	1604
Db	9943	TTTGCAAGAGAAATATTTAACAATATTTGGGTCCAACTTCAATATATATATATATAC	10002
Qy	1605	ATTATAAAGCATTTAATCTTCTTTCTAGAAATAATGCAAGGCTAAGGCATAGACAAACAA	1664
Db	10003	ATTATAAAGCATTTAATCTTCTTTCTAGAAATAATGCAAGGCTAAGGCATAGACAAACAA	10062
Qy	1665	AGAGAAATCGTGAAGAAATTTGCCACCTGAGACACAGCAATCTGAATTAATTTGCCAAA	1724
Db	10063	AGAGAAATCGTGAAGAAATTTGCCACCTGAGACACAGCAATCTGAATTAATTTGCCAAA	10122
Qy	1725	GTCTCTTTTATATGCAATATAGTGTGACAGATTTGAAGAGCTATTTTTTTTAAATGTTGCA	1784
Db	10123	GTCTCTTTTATATGCAATATAGTGTGACAGATTTGAAGAGCTATTTTTTTTAAATGTTGCA	10182
Qy	1785	CTACCAACTCATCTTGGAGAGACACAGCCAGAGATGGAAGTGAAGTGAAGTGAAGTGAAG	1844
Db	10183	CTACCAACTCATCTTGGAGAGACACAGCCAGAGATGGAAGTGAAGTGAAGTGAAGTGAAG	10242
Qy	1845	AATCATTTGTAGACATTTATGCCCATATAATTTAAATCAAGAAAATATGTGTATCTT	1904
Db	10243	AATCATTTGTAGACATTTATGCCCATATAATTTAAATCAAGAAAATATGTGTATCTT	10302
Qy	1905	TAGAAATTTGTATTCATCTTATATGACATATGTGACTATGCTTGTGATTAATTAAGC	1964
Db	10303	TAGAAATTTGTATTCATCTTATATGACATATGTGACTATGCTTGTGATTAATTAAGC	10362

QY 614 ATTTCCCTTTTCTGCGAGTTTGAAGATTAGAGAGATATGATGAAAAAGG 673
DB 481 ATTTCCCTTTTCTGCGAGTTTGAAGATTAGAGAGATATGATGAAAAAGG 540
QY 674 GAAGAAAGGAGAGAGAGAGAGTTAAAAAGTGTCTGAGACCTATGACGTATCC 733
DB 541 GAAGAAAGGAGAGAGAGAGTTAAAAAGTGTCTGAGACCTATGACGTATCC 600
QY 734 CTTTGCTGAAATTTTAAAGAGCTGAGCTTGTGAAACGAGTTTGTATCTTCC 793
DB 601 CTTTGCTGAAATTTTAAAGAGCTGAGCTTGTGAAACGAGTTTGTATCTTCC 660
QY 794 ATATTGAGAGAGATTTTCTGACTGCAATGCACTAGATGATTAATTTTATTT 853
DB 661 ATATTGAGAGAGATTTTCTGACTGCAATGCACTAGATGATTAATTTTATTT 720
QY 854 CATCTGAGAAAGCTTGTGATGAAAAATGAAATTTTGAAGGTTTCTGTCCATCT 913
DB 721 CATCTGAGAAAGCTTGTGATGAAAAATGAAATTTTGAAGGTTTCTGTCCATCT 780
QY 914 GGCCTGATGTCAGAGAGAGAGATGAAATGTAATCTCCATCCTCAAGCATCGA 973
DB 781 GGCCTGATGTCAGAGAGAGAGATGAAATGTAATCTCCATCCTCAAGCATCGA 840
QY 974 AACCCAAAGGAGTGAAGCAATTTCTATGATGATTTTGAAGATGATTTGTCATCTG 1033
DB 841 AACCCAAAGGAGTGAAGCAATTTCTATGATGATTTTGAAGATGATTTGTCATCTG 900
QY 1034 TATGCTGGCTCACTGCTATTAACCTCTGCTGATTAAGTCTTCTTATTTAGCA 1093
DB 901 TATGCTGGCTCACTGCTATTAACCTCTGCTGATTAAGTCTTCTTATTTAGCA 960
QY 1094 AGCAGTATCGAACAATTGCTTCCGACAGAGCTCTTATGATTAACATTTAGCACTATG 1153
DB 961 AGCAGTATCGAACAATTGCTTCCGACAGAGCTCTTATGATTAACATTTAGCACTATG 1020
QY 1154 TTTGTGTTAAACACATTTTCAACCAATAGTTTCTGAGGCAAGAGCAAGATGACTAT 1213
DB 1021 TTTGTGTTAAACACATTTTCAACCAATAGTTTCTGAGGCAAGAGCAAGATGACTAT 1080
QY 1214 TAAAGAAAGGCTTCCGACATCACTTCAATCCCAAACTAATAAAGATCACTTCC 1273
DB 1081 TAAAGAAAGGCTTCCGACATCACTTCAATCCCAAACTAATAAAGATCACTTCC 1140
QY 1274 AACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACGG 1333
DB 1141 AACTGAGAAAGACTCTGCTTGAATGAAACTTACAGAGAGTCAAGGCCACGG 1200
QY 1334 CAAGCAACAGCAACAACAATTGGAATTAATTCTCACTCACTGTTTATATA 1393
DB 1201 CAAGCAACAGCAACAACAATTGGAATTAATTCTCACTCACTGTTTATATA 1260
QY 1394 CATCTT-ATTAATTTTCTAGTAGAGAACTAACAATGACCTCTTCAACATTTATACA 1452
DB 1261 CATCTTATTAATTTTCTAGTAGAGAACTAACAATGACCTCTTCAACATTTATACA 1320
QY 1453 GTTTAATAAGCTCTTGAAGTACTTGTCTCTCACTGAGAGATTTTCTCCGCCA 1512
DB 1321 GTTTAATAAGCTCTTGAAGTACTTGTCTCTCACTGAGAGATTTTCTCCGCCA 1380
QY 1513 CTTGACCCCTGTCT 1572
DB 1381 CTTGACCCCTGTCT 1440
QY 1573 GGGTCCAACTTCAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1632
DB 1441 GGGTCCAACTTCAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1633 AAAATGCAAGGCTAGAGCATAGACAAAACAAGAAATGCTGAGAAATTTGCCACTGG 1692
DB 1501 AAAATGCAAGGCTAGAGCATAGACAAAACAAGAAATGCTGAGAAATTTGCCACTGG 1560

QY 1693 AGACAGCAATCTGAAATTAATTTTCCAAAAGTTCTTTTATGTCATATAGTCAGGA 1752
DB 1561 AGACAGCAATCTGAAATTAATTTTCCAAAAGTTCTTTTATGTCATATAGTCAGGA 1620
QY 1753 TTTGAGAGAGCTATTTTATTAATGTTGCAACTAGCACTCTTGGAGACACAGC 1812
DB 1621 TTTGAGAGAGCTA-TTTTATTAATGTTGCAACTAGCACTCTTGGAGACACAGC 1679
QY 1813 CAGAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1872
DB 1680 CAGAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1739
QY 1873 ATTTTAAATTCAGAAAAATTTGCTTTATCTTTGAAATTTGTAATCTTATGTA 1932
DB 1740 ATTTTAAATTCAGAAAAATTTGCTTTATCTTTGAAATTTGTAATCTTATGTA 1799
QY 1933 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1992
DB 1800 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1859
QY 1993 CACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2041
DB 1860 CACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1908

RESULT 8
ABV25337
ID ABV25337 standard; cDNA; 3461 BP.
XX AC ABV25337;
XX AC
XX DT 16-SEP-2002 (first entry)
XX XX
XX DE Human prostate expression marker CDNA 25328.
XX XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX XX
XX EN WO200160860-A2.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 20-FEB-2001; 2001WC-US005171.
XX XX
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX XX
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX XX
XX PI Schlegel R, Endege WO, Monahan JE;
XX XX
XX DR WPI; 2001-662795/76.
XX XX
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX XX
XX PS Claim 1; Page 4991-4992; 11750pp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC

XX Orr MS, Nation M, Diggins JC, Zeng W;
XX WPI; 2002-674803/72.
XX
XX Diagnosing breast cancer in a patient comprises detecting the level of
XX gene expression in cell or tissue samples, where a differential gene
XX expression is indicative of breast cancer.
XX
XX Claim 1; SEQ ID NO 257; 260bp + Sequence Listing; English.
XX
XX The present invention relates to methods of diagnosing breast cancer in a
XX patient, which comprise detecting the level of expression in a tissue
XX sample of two or more genes selected from those shown in ABR09867-
XX ABR1112, where a differential expression of the genes indicates breast
XX cancer. The methods are useful in diagnosing, treating, detecting the
XX progression, and in monitoring treatment of breast cancer in patients.
XX The methods are also useful as a screening tool for agents that modulate
XX the onset or progression of breast cancer. The breast cancer genes may be
XX used as diagnostic markers for the prediction or identification of the
XX malignant state of breast tissue, for confirming the type and progression
XX of cancer, and for drug screening and assays. The present sequence is a
XX coding sequence of the invention. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 594 BP; 204 A; 81 C; 110 G; 198 T; 0 U; 1 Other;
XX
XX Query Match 28.3%; Score 591.4; DB 6; Length 594;
XX Best Local Similarity 99.7%; Pred. No. 1.5e-113;
XX Matches 592; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1431 GCGCTTTCAACATTATATACAGTTAATAAGCCTCTGCAAGTACTGTTCTCTCAC 1490
DB 594 GCGCTTTCAACATTATATACAGTTAATAAGCCTCTGCAAGTACTGTTCTCTCAC 535
QY 1491 TGAGGATTTTCTCTCCGCCACCTGCGCCGTTCCCTCCCTCTCTCCCTTTGCA 1550
DB 534 TGAGGATTTTCTCTCCGCCACCTGCGCCGTTCCCTCTCTCTCTCTCTCTTGGCA 475
QY 1551 AGAGGAAATATTTAAATATTTGGTCCAACTCAATATATATATATATATATATTA 1610
DB 474 AGAGGAAATATTTAAATATTTGGTCCAACTCAATATATATATATATATATATTA 415
QY 1611 AGCATTTAATCT 1670
DB 414 AGCATTTAATCT 355
QY 1671 ATGCTGAGAAATTTTCCACTGAGAGCAAGCAATCTGAATTAATATTTGCCAAAGTCTT 1730
DB 354 ATGCTGAGAAATTTTCCACTGAGAGCAAGCAATCTGAATTAATATTTGCCAAAGTCTT 295
QY 1731 TTTAATGTCAT 1790
DB 294 TTTAATGTCAT 235
QY 1791 ACTGATCTTGGAGAGACAGCAGAGAGATGAAGTGAAGTGAAGTGAAGTGAAGTGA 1850
DB 234 ACTGATCTTGGAGAGACAGCAGAGAGATGAAGTGAAGTGAAGTGAAGTGAAGTGA 175
QY 1851 TTTGTAAGCAATTTATCCATATATATATATATATATATATATATATATATAT 1910
DB 174 TTTGTAAGCAATTTATCCATATATATATATATATATATATATATATATATAT 115
QY 1911 TTTGTAATCAATTTAT 1970
DB 114 TTTGTAATCAATTTAT 55
QY 1971 TATGATCTGTAACCAATCAATCAATATATATATATATATATATATATATATAC 2024
DB 54 TATGATCTGTAACCAATCAATCAATATATATATATATATATATATATATATAC 1

RESULT 10
ABX74748
ID ABX74748 standard; cDNA; 488 BP.
XX
XX AC ABX74748;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human cDNA sequence #1 up-regulated in CC-RCC patients.
XX
XX KW Human; microarray; solid surface; immobilised probe; CC-RCC;
XX differential expression profile; aggressive CC-RCC tumour type;
XX non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
XX KW gene expression profiling; tumour tissue; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN NC0200279411-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002MO-US009576.
XX
XX PR 29-MAR-2001; 2001US-0279411P.
XX
XX PA (VAND-) VAN ANDEL INST.
XX
XX PI Haab B, Rhodes D, Teh BT, Takashi M,
XX
XX DR WPI; 2003-040679/03.
XX
XX PT New microarray comprising a matrix of cDNA probe from a set of probes
XX immobilised to a solid surface in predetermined order, useful in the
XX prognosis of patients with clear cell renal carcinoma.
XX
XX PS Claim 35; SEQ ID NO 141; 179bp; English.
XX
XX The present invention relates to a microarray comprising a matrix of at
XX least one cDNA probe from a set of probes immobilised to a solid surface
XX in a predetermined order, where a row of pixels corresponds to replicates
XX of one distinct probe from the set. The probes are complementary to
XX nucleic acid sequences that are expressed differentially in aggressive as
XX compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)
XX and that hybridise to the probes under high stringency conditions. The
XX microarray is useful for the prognosis of patients with CC-RCC, wherein
XX aggressive and non-aggressive CC-RCC tumour types are characterised by
XX differential expression profiles of genes that hybridise with one or more
XX probes immobilised on the microarray. The arrays are useful for gene
XX expression profiling of tumour and normal tissues. The present sequence
XX represents a human cDNA sequence up-regulated in CC-RCC patients
XX
XX Sequence 488 BP; 151 A; 122 C; 69 G; 145 T; 0 U; 1 Other;
XX
XX Query Match 20.4%; Score 425.8; DB 7; Length 488;
XX Best Local Similarity 98.6%; Pred. No. 4.5e-79;
XX Matches 482; Conservative 0; Mismatches 2; Indels 5; Gaps 5;
XX
QY 1070 ATAGTCTCTTCATTTATAGACAGACGATGCAACTTGGCTTGGACAAAGCTCTT 1129
DB 2 ATAGTCTCTTCATTTATAGACAGACGATGCAACTTGGCTTGGACAAAGCTCTT 60
QY 1130 TAGTTAAACAATTTAGAGAGCTAGTGTGTGTTAAACAACACTTTTCCAAATAGTCTG 1189
DB 61 TAGTTAAACAATTTAGAGAGCTAGTGTGTGTTAAACAACACTTTTCCAAATAGTCTG 120
QY 1190 AGGCAAAAG 1249
DB 121 AGGCAAAAG 180
QY 1250 AAAAATGAAAG 1309
DB 181 AAAAATGAAAG 240

Db 362 TACTTCATACCCGCTACTCAATTCCTACTGATGATTAAGCTTTAACTAAT 421
 QY 285 TCAGTGCCAGAGAACTTGTAATTAATTAATTTTAAATTTTAAAT 335
 Db 422 TCAGTGCCAGAGAACTTGTAATTAATTAATTTTAAATTTTAAAT 422

RESULT 15

AA883630
 ID AA883630 standard; cDNA; 1584 BP.

AC AA883630;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19434.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PA 23-AUG-2000; 2000US-00649167.

PI (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG19443.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 1; SEQ ID NO 19434; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA864197-AA89464 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 1584 BP; 456 A; 331 C; 370 G; 422 T; 0 U; 5 Other;

Query Match 9.3%; Score 194.2; DB 5; Length 1584;
 Best Local Similarity 97.2%; Pred. No. 1e-30;
 Matches 207; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1748 CAGGATTTGAGAGAGCTATTTTTTTAAATGTTGCACTAGCACTCATCTTGGAGAGC 1807
 Db 1373 CAGGATTTGAGAGAGCTATTTTTTTAAATGTTGCACTAGCACTCATCTTGGAGAGC 1432
 QY 1808 ACAGCCAGAGAGATGAGTAGAGTGAAGGTTTAAATTCATTGTAAGCATTTATCC 1867
 Db 1433 ACAGCCAGAGAGATGAGTAGAGTGAAGGTTTAAATTCATTGTAAGCATTTATCC 1492
 QY 1868 CATATATTTTAAATTCAGAAAAATTTGTTATCTTTAGAAATTTGATTCATATCTTT 1927
 Db 1493 CATATATTTTAAATTCAGAAAAATTTGTTATCTTT-GAATTTGATTCATATCTTT 1551
 QY 1928 ATGTAATATGTAAGTCACTGCTCTGATTAATA 1960
 Db 1552 ATGTAATATGTAAGTCACTGCTCTGATTAATA 1584

Search completed: May 5, 2004, 14:13:14
 Job time : 825 secs

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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 12:48:38 ; Search time 8111 Seconds

(without alignments)
11173.750 Million cell updates/sec

Title: US-09-646-569A-60

Perfect score: 1 aagagacagactatcattc.....gagagagaggggggaggt 2091

Sequence: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Scoring table: 3470272 segs, 2167151695 residues

Searched: Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_da.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vt.*

15: em_da.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vt.*

30: em_hcg_hum.*

31: em_hcg_inv.*

32: em_hcg_other.*

33: em_hcg_mus.*

34: em_hcg_dln.*

35: em_hcg_rtd.*

36: em_hcg_mam.*

37: em_hcg_vrt.*

38: em_sy.*

39: em_hcgo_hum.*

40: em_hcgo_mus.*

41: em_hcgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2091	100.0	2091	6	AX017512	AX017512 Sequence
2	2091	100.0	2091	6	BD135202	BD135202 Human nuc
3	2036	97.4	2411	6	AX017611	AX017611 Sequence
4	2036	97.4	2411	6	BD135230	BD135230 Human nuc
5	2003.6	95.8	3674	6	BD218591	BD218591 71 human
6	2001.2	95.7	5683	9	HS0805729	BX537427 Homo sapi
7	2000.6	95.7	191699	2	AC031977	AC031977 Homo sapi
8	1997.4	95.5	165329	9	AL583850	AL583850 Human DNA
9	1878.6	89.8	1909	6	AX393338	AX393338 Sequence
10	1853.4	88.6	6005	6	AR379796	AR379796 Sequence
11	1845.6	88.3	1863	9	AK026775	AK026775 Homo sapi
12	1225.6	58.6	1490	9	BC029357	BC029357 Homo sapi
13	1112	53.2	1121	9	HS0802503	AL157502 Homo sapi
14	331	15.8	331	6	AX330124	AX330124 Sequence
15	331	15.8	331	6	AX334654	AX334654 Sequence
16	331	15.8	331	6	AX408713	AX408713 Sequence
17	210	10.0	224486	2	AC115766	AC115766 Mus muscu
18	160.4	7.7	21316	10	BC005656	BC005656 Mus muscu
19	155	7.4	27531	2	AC125563	AC125563 Rattus no
20	136	6.5	140	6	AX901039	AX901039 Sequence
21	136	6.5	140	6	BD036572	BD036572 Sequence
22	95.2	4.6	547	6	AX401089	AX401089 Sequence
23	74.8	3.6	229692	2	BX649311	BX649311 Danio rer
24	70	3.3	110000	2	PF0413_00	AL844509 Plasmodi
25	69	3.3	176785	2	AC116848	AC116848 Mus muscu
26	68.8	3.3	277530	2	BX572620	BX572620 Danio rer
27	67.6	3.2	18138	2	BX664607	BX664607 Danio rer
28	67.2	3.2	103344	9	HS1100E15	AL035551 Human DNA
29	67.2	3.2	182477	2	BX649274	BX649274 Danio rer
30	67.2	3.2	252420	3	AE014841	AE014841 Plasmodi
31	66.8	3.2	212487	2	BX649365	BX649365 Mus muscu
32	66.6	3.2	21208	3	PRG27	X84904 Plasmodi
33	66.2	3.2	170131	2	BX666066	BX666066 Danio rer
34	65.8	3.1	347582	3	PF0414_1	AL034557 Plasmodi
35	65.4	3.1	301	6	BD242186	BD242186 Compounds
36	65.4	3.1	301	6	AR337369	AR337369 Sequence
37	65.4	3.1	301	6	AR3260862	AR3260862 Sequence
38	65.4	3.1	301	6	AR278393	AR278393 Sequence
39	65.4	3.1	301	6	AR367089	AR367089 Sequence
40	65.4	3.1	301	6	AR370985	AR370985 Sequence
41	65.4	3.1	301	6	AR392490	AR392490 Sequence
42	65.4	3.1	301	6	AR400125	AR400125 Sequence
43	65.4	3.1	301	6	AR405392	AR405392 Sequence
44	65.4	3.1	301	6	AX106499	AX106499 Sequence
45	65.4	3.1	301	6	AX140790	AX140790 Sequence

ALIGNMENTS

RESULT 1

AX017512

LOCUS

DEFINITION

AX017512

ACCESSION

VERSION

AX017512.1 GI:10042309

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pilarsky, C.

TITLE

Human nucleic acid sequences from normal breast tissue

2091 bp DNA linear PART 07-SRP-2000

Db 1321 TCACAGGCCAGCGCAACAAACAACACAAACATTGGAAATATTATCTCACTCA 1380
QY 1381 CGTTTAAATATACATCTTATTATTTTCTAGTAGAAGAACTACAAATCAGCCTTCA 1440
Db 1381 CGTTTAAATATACATCTTATTATTTTCTAGTAGAAGAACTACAAATCAGCCTTCA 1440
QY 1441 CATTATATACAGTTTAAATAGCCTTCTGAAAGTTACCTGTTCTCTCACCTGAGTTAT 1500
Db 1441 CATTATATACAGTTTAAATAGCCTTCTGAAAGTTACCTGTTCTCTCACCTGAGTTAT 1500
QY 1501 TTTTCTCCGCACTTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
Db 1501 TTTTCTCCGCACTTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
QY 1561 TTTTACATATTTGGGTCCAACTTCAATATATATATATATATATATATATATATAT 1620
Db 1561 TTTTACATATTTGGGTCCAACTTCAATATATATATATATATATATATATATATAT 1620
QY 1621 TTCTCTCTAGAAATATGACAGGCTAGAGCATAGACAAACAAAGAGAAATGCTGAGA 1680
Db 1621 TTCTCTCTAGAAATATGACAGGCTAGAGCATAGACAAACAAAGAGAAATGCTGAGA 1680
QY 1681 ATTGCACTGAGACAGCAATCTGAATATAATTGCAAAAGTTCTTTTATGTCAT 1740
Db 1681 ATTGCACTGAGACAGCAATCTGAATATAATTGCAAAAGTTCTTTTATGTCAT 1740
QY 1741 ATATGTCAGAGATTTAGAGAGCTATTTTATATATGTTGCACTAGCACTCATCTTC 1800
Db 1741 ATATGTCAGAGATTTAGAGAGCTATTTTATATATGTTGCACTAGCACTCATCTTC 1800
QY 1801 GGAAGACAGCAGCAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 GGAAGACAGCAGCAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 TTTATCCCATATTTTAAATTCAGAAATTTGTTTATCTTATGAAATTTTGTATCA 1920
Db 1861 TTTATCCCATATTTTAAATTCAGAAATTTGTTTATCTTATGAAATTTTGTATCA 1920
QY 1921 ATACTTAT 1980
Db 1921 ATACTTAT 1980
QY 1981 TAAACCAATGACACAT 2040
Db 1981 TAAACCAATGACACAT 2040
QY 2041 AGAAG 2091
Db 2041 AGAAG 2091

RESULT 3
AX017611 2411 bp DNA linear PART 07-SEP-2000
LOCUS Sequence 175 from Patent WO947655.
DEFINITION AX017611
ACCESSION AX017611 GI:10042337
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Schmitz, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pillarsky, C.
TITLE Human nucleic acid sequences from normal breast tissue
JOURNAL Patent: WO 947655-A 175 23-SEP-1999;
SCHEMITZ, A.; SPECHT, T.; DAHL, E.; HINZMANN, B.; ROSENTHAL, A.; PILLARSKY, C.; METZGER, G. GENOMFORSCHUNG

FEATURES
source 1. 2411 /organism="Homo sapiens"

ORIGIN
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 97.4%; Score 2036; DB 6; Length 2411;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2081; Conservative 0; Mismatches 10; Indels 19; Gaps 2;

QY 1 AAGAGACAGCTATTAACCTGACAGTTAATTAAGACGATAGTTCATGTTTATTTGTTA 60
Db 302 AAGAGACAGCTATTAACCTGACAGTTAATTAAGACGATAGTTCATGTTTATTTGTTA 361
QY 61 AAGAGAGTAAATAGCCTCAAGCATGTAATATCTTCATGTTCCCGC----- 111
Db 362 AAGCAGTGTAATAGCCTCAAGCATGTAATATCTTCATGTTCCCGCAGACATAC 421
QY 112 -----CGCTTTTGTCTTTCAGGTAGACCTTTTAAATGACAACTAAGT 164
Db 422 ACAACACACTTTTGTCTTTCAGGTAGACCTTTTAAATGACAACTAAGT 481
QY 165 CATTTCGTAACCTTGTCTTCAATGATTAATTAAGTCAAAATGTAAGAACTATTTGTC 224
Db 482 CATTTCGTAACCTTGTCTTCAATGATTAATTAAGTCAAAATGTAAGAACTATTTGTC 541
QY 225 TACTCTCATACCCCGTGTACTCAATTCCTCTAGTATGATTAATGCTTTAAGTAAT 284
Db 542 TACTCTCATACCCCGTGTACTCAATTCCTCTAGTATGATTAATGCTTTAAGTAAT 601
QY 285 TCACTGCCAAGAGAACTTGTGTAATTAATTTTATTTTATCTTTTATCTTTACAA 344
Db 602 TCACTGCCAAGAGAACTTGTGTAATTAATTTTATTTTATCTTTTATCTTTACAA 661
QY 345 AGCCATGATTTTATTTGTTGATGATGCTGTACACAGCCATTTCAATAGATGA 404
Db 662 AGCCATGATTTTATTTGTTGATGATGCTGTACACAGCCATTTCAATAGATGA 721
QY 405 GCTGTATATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGATG 464
Db 722 GCTGTATATTTTCCAAAGATTAATGATGATGATGATGATGATGATGATGATGATG 781
QY 465 TTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 524
Db 782 TTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 841
QY 525 TCCATTAACAATTTTGAATCGTTGAATAGCTGATTAATTTTCAAGAAATGATTTTC 864
Db 842 TCCATTAACAATTTTGAATCGTTGAATAGCTGATTAATTTTCAAGAAATGATTTTC 901
QY 585 ATATTTGAATCTGTTCCCTAGAGGCAATTTTCCCTTTTCTGGAGTTTAGCAAT 644
Db 902 ATATTTGAATCTGTTCCCTAGAGGCAATTTTCCCTTTTCTGGAGTTTAGCAAT 961
QY 645 TTAAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 704
Db 962 TTAAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1021
QY 705 GTAAGTCTGACGCTTGAAGCTAATCCCTTGTCTGAATATTTTGAAGAGCTGAC 764
Db 1022 GTAAGTCTGACGCTTGAAGCTAATCCCTTGTCTGAATATTTTGAAGAGCTGAC 1081
QY 765 TTGCTTGAATCTGATTTTGTCAATCTTCAATTTTGAAGAGATTTTCTGACTGCA 824
Db 1082 TTGCTTGAATCTGATTTTGTCAATCTTCAATTTTGAAGAGATTTTCTGACTGCA 1141
QY 825 ATGACGCTAATGTAATTTTATTTTATATATATATATATATATATATATATATAT 884
Db 1142 ATGACGCTAATGTAATTTTATTTTATATATATATATATATATATATATATATAT 1201
QY 885 TAAATATTTGAGGTTTCTGCTCAATCTGCTTGTGACATGTCAGAAAGCAAGAAATGA 944
Db 1202 TAAATATTTGAGGTTTCTGCTCAATCTGCTTGTGACATGTCAGAAAGCAAGAAATGA 1261
QY 945 AAATGTAATCTCCCAATCCCAAGATGAAACCAAGGGTGAAGCAATTTCTATGATG 1004

Db	1262	AAATGTATATCTCCAAATCCAGATCGAAACCCAAAGGGCTATGGCAATTCATATAGGTT	1321
QY	1005	TTGGACATGAAAGTTGGTGCAATCTTGTTATAGCTGCTCACTGCTATTTAACTCTCT	1064
Db	1322	TTGGACATGAAAGTTGGTGCAATCTTGTTATAGCTGCTCACTGCTATTTAACTCTCT	1381
QY	1065	GGCTTATAGCTCTTCAATCTATTTAGACAAACAGTATCGAAACCTTGCTCGACAAAG	1124
Db	1382	GGCTTATAGCTCTTCAATCTATTTAGACAAACAGTATCGAAACCTTGCTCGACAAAG	1441
QY	1125	CTCTTTAGTTAACATTTTTCAGAGCTACTGTTGTGTTTAAACACTTTTCCAAATAG	1184
Db	1442	CTCTTTAGTTAACATTTTTCAGAGCTACTGTTGTGTTTAAACACTTTTCCAAATAG	1501
QY	1185	TTTCGAGGCAACGAGAGCAATGACTATTTTAAAGAGCTTTCGAGCACTTAC	1244
Db	1502	TTTCGAGGCAACGAGAGCAATGACTATTTTAAAGAGAGCTTTCGAGCACTTAC	1561
QY	1245	ATCCCAAACTTAAAGAAAGATCACTCTTCCACTGAGAAAGACTCTGGCTTGAATGA	1304
Db	1562	ATCCCAAACTTAAAGAAAGATCACTCTTCCACTGAGAAAGACTCTGGCTTGAATGA	1621
QY	1305	AACCTTACGACGAGAGTCAACGCGCACGCGCAACACGACACACAAACATTTGGA	1364
Db	1622	AACCTTACGACGAGAGTCAACGCGCACGCGCAACACGACACACAAACATTTGGA	1681
QY	1365	TATATTTCTCACTCAGCTTTTAAATTAATACATCTATATTTCTTACTAGAGAACTAC	1424
Db	1682	TATATTTCTCACTCAGCTTTTAAATTAATACATCTATATTTCTTACTAGAGAACTAC	1741
QY	1425	AAATCAGCTCTTCAACATTTATATATACGTTTAAATAGCTCTTGCAAGTTACTGTCT	1484
Db	1742	AAATCAGCTCTTCAACATTTATATATACAGTTTAAATAGCTCTTGCAAGTTACTGTCT	1801
QY	1485	CTCAGCTGAGGATTTTTTTTCTCCGCCACCTGGCCCGCTCCGCCCTCTCTCC	1544
Db	1802	CTCAGCTGAGGATTTTTTTTCTCCGCCACCTGGCCCGCTCCGCCCTCTCTCTCC	1861
QY	1545	TTTGCAAGAGAAATATTTAACATATTTGGGTCCAACTTCATATATGTAATTAATTAAC	1604
Db	1862	TTTGCAAGAGAAATATTTAACATATTTGGGTCCAACTTCATATATGTAATTAATTAAC	1921
QY	1605	ATTTAAAGCATTTTAACTCTCTTTCTAGAAAAATGCAAGGCTTAAGGCTAAGCAAAACA	1664
Db	1922	ATTTAAAGCATTTTAACTCTCTTTCTAGAAAAATGCAAGGCTTAAGGCTAAGCAAAACA	1981
QY	1665	AGAGAAATGCTGAGAAATTTGCGACTGAGACAAGCAATCTGAATTAATTTTGCAAAA	1724
Db	1982	AGAGAAATGCTGAGAAATTTGCGACTGAGACAAGCAATCTGAATTAATTTTGCAAAA	2041
QY	1725	GTTCTTTTATGTCATATATAGTGTGTCAGATTTGAAAGAGCTATTTTTTTTATGTTGCA	1784
Db	2042	GTTCTTTTATGTCATATATAGTGTGTCAGATTTGAAAGAGCTATTTTTTTTATGTTGCA	2101
QY	1785	CTAGAAATCATCTTCGGAAGACACAGCAGAGAAATGAATGAGAGGAAGGTTTATA	1844
Db	2102	CTAGAAATCATCTTCGGAAGACACAGCAGAGAAATGAATGAGAGGAAGGTTTATA	2161
QY	1845	AATCATTGTGTAAGCATTTATCCATATATTTTAAATTCAGAAAAATTGTTATGTTCT	1904
Db	2162	AATCATTGTGTAAGCATTTATCCATATATTTTAAATTCAGAAAAATTGTTATGTTCT	2221
QY	1905	TAGAAATTTTGTATTAATTAATTTTATAGTACTATGACATCAAGCTCTCGAATTAAGC	1964
Db	2222	TAGAAATTTTGTATTAATTAATTTTATAGTACTATGACATCAAGCTCTCGAATTAAGC	2281
QY	1965	ACCAATATATGATCTGTAAACCAATCAACATATATATTAATTAATATATCTATATAC	2024
Db	2282	ACCAATATATGATCTGTAAACCAATCAACATATATATTAATTAATATATCTATATAC	2341
QY	2025	AGCCAAAAAAGAAAAAGAG--GAGAAAAAGAAAGAGGGGGGGGAGAGAGG	2081

Db	2242	AGCGCAAAAAAAAAAAAAAAAAA	CACAGAAAAAAGGAGAGGCGGCGAAGAAAG	2401
Qy	2082	GGGGGGAGGT	2091	
Db	2402	GGGGGGAGGT	2411	
RESULT 4				
LOCUS	BD135230	2411 bp	DNA	linear
DEFINITION	Human nucleic acid sequence originating in normal mammary tissue.			
ACCESSION	BD135230			
VERSION	BD135230.1	GI:23230175		
KEYWORDS	JP 2002050639-A/77.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 2411) Speft,T., Hantzman,B., Shemitt,A., Pirarski,C., Duhl,E. and Rosenthal,A.			
TITLE	Human nucleic acid sequence originating in normal mammary tissue			
JOURNAL	Patent: JP 2002050639-A-77 05-MAR-2002; MERGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH			
COMMENT	OS Homo sapiens (human) PN JP 2002050639-A/77 PD 05-MAR-2002 PF 19-MAR-1999 JP 2000536838 PR 20-MAR-1998 DE 198 13 835.0 PI THOMAS SPEFT, BERND HINTZMAN, ARWIN SHCMITT, CHRISTIAN PIRARSKI, PI EDGAR DUHL, PI ANDRE ROSENTHAL PC C12N15/09,A61K48/00,A61E35/00,A61P43/00,C07K14/47, PC C07K16/18, PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//A61K38/00, PC C12N15/00, PC C12N5/00,A61K37/02 CC Human nucleic acid sequence originating in normal mammary tissue			
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ORIGIN				
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Match Local Similarity	98.6%; Pred. No. 0;			
Matches 2081; Conservative	0; Mismatches 10; Indels 19; Gaps 2			
Qy	1	AAGAGACAGACTAATTAATCTCCACAGTTAATTAAAGACGATGTTCCATGTTATTGTTA	60	
Db	302	AAGAGACAGACTAATTAATCTCCACAGTTAATTAAAGACGATGTTCCATGTTATTGTTA	361	
Qy	61	AAGAGAGTGTAATGACCTTCAAGATGGAATTAATCTCCATCTTCCCGC-----	111	
Db	362	AAGCAGGTGTAATGACCTTCAAGATGGAATTAATCTCCATCTTCCCGC	421	
Qy	112	-----CGCTTTTGTGTTCTTTTCAGGTAGACACCTTTTAAATGACAGAACTTAAGG	164	
Db	422	ACACACACACTTTTGTGTTCTTTTCAGGTAGACACCTTTTAAATGACAGAACTTAAGG	481	
Qy	165	CATTTCGATACTTGCCTTCAATCAATAAGCAATGATGGAACATTTGTGCC	224	
Db	482	CATTTCGATACTTGCCTTCAATCAATAAGCAATGATGGAACATTTGTGCC	541	
Qy	225	TACTCTCATATCCCGGTGTACTCAAAATTCCTTACTGATGAATTAATGCTTTAAGTAGAT	284	
Db	542	TACTCTCATATCCCGGTGTACTCAAAATTCCTTACTGATGAATTAATGCTTTAAGTAGAT	601	

[illegible]

Db	1682	TATATTCTCACTCAGCTTTTAAATACATCTTTATATTTTCTAGTAGAAGAACTAC	1741
QY	1425	AAATCAGCCCTTCAACATTTATATACAGTTTAAATAGCCTCTTGCAAGTACTTGTTCT	1484
Db	1742	AAATCAGCCCTTCAACATTTATATACAGTTTAAATAGCCTCTTGCAAGTACTTGTTCT	1801
QY	1485	CTCAGCTGAGATATTTTTTCCCTCCCACTTCGCCCTGTCCTCCCTCCCTCTCTCCG	1544
Db	1802	CTCAGCTGAGATATTTTTTCCCTCCCACTTCGCCCTGTCCTCCCTCCCTCTCTCCG	1861
QY	1545	TTTGCAAGAGAAATATTTTAACTATTTTGGTCCAACTTCAATATATATATATATAC	1604
Db	1862	TTTGCAAGAGAAATATTTTAACTATTTTGGTCCAACTTCAATATATATATATATAC	1921
QY	1605	ATTAAAGCAATTTAATCTTCTTTCTAGAAAAATGCAAGGCTAAGCATAGACAAAAACA	1664
Db	1922	ATTAAAGCAATTTAATCTTCTTTCTAGAAAAATGCAAGGCTAAGCATAGACAAAAACA	1981
QY	1665	AGGAATGCTGAGAAATTTGCACTGAGACAAGCATCTGAATTAATTTTGCCAAA	1724
Db	1982	AGGAATGCTGAGAAATTTGCACTGAGACAAGCATCTGAATTAATTTTGCCAAA	2041
QY	1725	GTCTCTTTTATGTCATATAGTGTGAGATTTGAAAGAGCTATTTTTTTTAAATGTCGA	1784
Db	2042	GTCTCTTTTATGTCATATAGTGTGAGATTTGAAAGAGCTATTTTTTTTAAATGTCGA	2101
QY	1785	CTAGCACTGATCTTGGAAGACAAGCAGCAGGAATGAGATGAGATGAAAGGTTTATA	1844
Db	2102	CTAGCACTGATCTTGGAAGACAAGCAGCAGGAATGAGATGAGATGAAAGGTTTATA	2161
QY	1845	AATCATTGTTGAGCATTTTATCCCATATATTTTAAATTCAGAAAAATTTGTTTACTT	1904
Db	2162	AATCATTGTTGAGCATTTTATCCCATATATATTTTAAATTCAGAAAAATTTGTTTACTT	2221
QY	1905	TAGAAATTTGATTCATATCTTTATGACATATGCACTCATGCTCTCGAATTAATAAGC	1964
Db	2222	TAGAAATTTGATTCATATCTTTATGACATATGCACTCATGCTCTCGAATTAATAAGC	2281
QY	1965	ACCAATATGATCTGTACCAACATCAATCATATTTAATTAATATATATCTATATAC	2024
Db	2282	ACCAATATGATCTGTACCAACATCAATCATATTTAATTAATATATATCTATATAC	2341
QY	2025	AGCCAAAAAAG	2081
Db	2342	AGCCAAAAAAG	2401
QY	2082	GGGGGGAGGT 2091	
Db	2402	GGGGGGAGGT 2411	
RESULT 5			
BD218591	BD218591	3674 bp	DNA linear
LOCUS	BD218591		
DEFINITION	71 human secretory proteins.		
ACCESSION	BD218591		
VERSION	BD218591.1		
KEYWORDS	JP 2002520050-A/72.		
SOURCE	Human sapiens (human)		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eubacteria; Primates; Carnivora; Hominiidae; Homo.		
AUTHORS	1 (baaes 1 to 3674) Rumen,S.M., Komatsoulis,G., Duan,R.D., Rosen,C.A., Moore,P.A., Shl,Y., Lafleur,D.W., Ebner,R., Olsen,H.S., Brewer,L.A., Florence,K.A., Young,P.E., Mucenik,W., Endresek,G.A. and Soppel,D.R.		
TITLE	71 human secretory proteins		
JOURNAL	Patent: JP 2002520050-A 72 09-JUL-2002;		
COMMENT	HUMAN GENOME SCIENCES INC OS Homo sapiens (human) PN JP 2002520050-A/72		

PD 09-JUL-2002
PF 14-JUL-1999 JP 2000560238
PR 15-JUL-1998 US 60/092921,15-JUL-1998 US 60/092922 PR
15-JUL-1998 US 60/092956
PI STEVEN M RUBEN, GEORGE KOMATSOUIS, ROXANNE
D DUAN, CRAIG A ROSEN,
PI PAUL A MOORE, YANQU SHI, DAVID W LAFLEUR, REINHARD EBNER, HENRIK
PI S OLSEN,
PI LAURIE A BREWER, KIMBERLY A FLORENCE, PAUL E YOUNG, MICHAEL PI
MUCENSKI,
PI GREGORY A ENDESS, DANIEL R SOPPET
PC C12N15/09, C07H21/02, C07H21/04, C07K16/47, C07K16/18, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, G01N33/50, G01N33/68//C12Q1/68, PC
C12N15/00,
PC C12N5/00
CC 71 human secretory proteins
FH Key Location/Qualifiers
FT source 1.3674
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ORIGIN
Query Match 95.8%; Score 2003.8; DB 6; Length 3674;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2034; Conservative 0; Mismatches 7; Indels 16; Gaps 1;

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1677 AAGAGAGTGAATAGCTTCAAGCATGTGAATTAATCTCCAGTGAATTTGTCGCGC-----1736
112 -----CGCTTTGTTGTTCTTCAAGTGAATCACTTTTAAAGCAGAACTAATGAG 164
1737 AACAACACACTTTGTTGTTCTTCAAGTGAATCACTTTTAAAGCAGAACTAATGAG 1796
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1797 CATTGAGTAACTTGTCTTCAATCAATTAAGTCAATGATGAGAAACATTTGTCGCC 1856
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Db	3357	GTCTTTTAAAGTCATATAGTGTAGAGATTGAAGAGACATTTTCTTTTAAAGTGCAA	3416
QY	1785	CTAGCAACTCATCTTTCGGAGACACACGCCAGAGAAATGAGTGAAGTGAAGGTTATA	1844
Db	3417	CTAGCAACTCATCTTTCGGAGAGACACAGAGAAATGAGTGAAGTGAAGGTTATA	3476
QY	1845	AATGCATTGTAGAGATTATCCCATATATTTTAAATTCAGAAAAATTTGGTTATCTT	1904
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QY	1905	TAGAAATTTGTATTCATTAATCTTTATGTACATATGTGACTCATGCTTCTGGATAAATTAAGC	1964
Db	3537	TAGAAATTTGTATTCATTAATCTTTATGTACATTAATGTGACTCATGCTTCTGGATAAATTAAGC	3596
QY	1965	ACCAAAATGTATATCGTGTACCAACAATCACAATATATATTAATTAATATATATATATATATAC	2024
Db	3537	ACCAAAATGTATATCGTGTACCAACAATCACAATATATATATTAATTAATATATATATATATAC	3656
QY	2025	AGCCAAAAATTTTTAAAAA 2041	
Db	3657	AAAAAAAAAAAAAAAAAAAA 3673	
RESULT 6			
LOCUS	HSMB05729	5663 bp	mRNA linear PRI 16-JUN-2003
DEFINITION	Homo sapiens mRNA; CDNA DKFPZ686G1211 (from clone DKFPZ686G1211); complete cds.		
ACCESSION	BX37427		
VERSION	BX37427.1	GI:31873355	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 5683) Bloeker,H., Boecker,M., Mewes,H.W., Well,B., Aml,D.C., Oeanger,A., Fodor,G., Han,M. and Wiemann,S. Direct Submission Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY		
TITLE	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.		
JOURNAL	This clone (DKFPZ686G1211) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.		
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QY	885	TAAATATTGAGGGTTTCCTGTCATATCTG3CTTGCACTGTCGCGAAGAAACAGAGATAGA	944
Db	4528	TAAATATTGAGGGTTTCCTGTCATACTG6CTTGCACTGTCGCGAAGAAAGCAGAAATAGA	4587
QY	945	AAATGTATCTCCCAACTCCAGAGATGAAACCCAGAGGGGTAGGCAATCTATAGAGTT	1004
Db	4588	AAATGTATCTCCCAACTCCAGAGATGAAACCCAGAGGGGTAGGCAATCTATAGAGTT	4647
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Db	4648	TTGCACATGAAGTTTGGTGCACTTGGTTTATGCTGGCTCACTGCTATTAACTCTCT	4707
QY	1065	GGCTTATAGTCTCTTCACTTCTATTAGACAAGACAGTATCGAACACTGTGCTTGCACAAAG	1124
Db	4708	GGCTTATAGTCTCTTCACTTCTATTAGACAAGACAGTATCGAACACTGTGCTTGCACAAAG	4767
QY	1125	CTCTTTAGTAAACATTTTAGAGCTACTGTTTGTATTAACACACTTTTACCAAAATAG	1184
Db	4768	CTCTTTAGTAAACATTTTAGAGCTACTGTTTGTATTAACACACTTTTACCAAAATAG	4827
QY	1185	TTCTGAGCGCAACGAGAGCAATGACATTTTAAAGAAAGGCTTCCGACATCACTTACAC	1244
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QY	1245	ATCCCAAACTTAAAAAAGTCAACTCTTCGAACTGAGAAAAGACTCTGGCTTTGAATGA	1304
Db	4888	ATCCCAAACTTAAAAAAGTCAACTCTTCGAACTGAGAAAAGACTCTGGCTTTGAATGA	4947
QY	1305	AACTTACAGCAGAGAGTCACAGGCGCACGCAACAACGACAAACAACAATTTGGAA	1364
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QY	1365	TATATCTCTCACTCAAGTTTATATATATATATATATATTTTCTATGAGAGAACTAC	1424
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QY	1425	AAATCAGCCTCTTCAACATTTATATATACAGTTTAAAGCCCTTGCAGATTACTGTCT	1484
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Db	5128	CTCACCAGGATATTTTCTTCTCCGCCACCTTGCCCGCTGTCCTCCCTCCTCTCCC	5187
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Db	5308	AGAGAAATGCTGAGAAATTTTGCACCTGAGACAAGCAATCTGAATTAATTTTCCCAAA	5367
QY	1725	GTTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTTTTTATATGTTGCA	1784
Db	5368	GTTCTTTTATGTCATATATAGTGTCAAGATTTGAAGAGCTATTTTTTTTATATGTTGCA	5427
QY	1785	CTAGCAACTCATCTTCCGAGAACACAGCAGAGAGATAGATAGAGGAAAGGTTTATA	1844
Db	5428	CTAGCAACTCATCTTCCGAGAACACAGCAGAGAGATAGATAGAGGAAAGGTTTATA	5487
QY	1845	AATCCATTTGTAAGCATTTATCCATATATTTTAAATTCAGAAAAATTTGTATTACTT	1904
Db	5488	AATCCATTTGTAAGCATTTATCCATATATTTTAAATTCAGAAAAATTTGTATTACTT	5547
QY	1905	TAGATATTTGTTATTCATATCTTTATATGTAATAGTACACAGCTCTGAGATTAATTAAGC	1966
Db	5548	TAGATATTTGTTATTCATATCTTTATATGTAATAGTACACAGCTCTCTGAGATTAATTAAGC	5607

QY 1365 ACCGAAATATCTATCTGTGAACACAACTACACACATTTATTAATATATCTCTATTAAC 2024
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QY 2025 AGCCGAAAAAAAAAAAA 2040
Db 5668 AAAAAAAAAAAAAACA 5683

RESULT 7	
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LOCUS	191699 bp DNA linear HTG 12-APR-2001
DEFINITION	Homo sapiens chromosome 1 clone RP11-288018, WORKING DRAFT
SEQUENCE	3 unordered pieces.

ACCESSION	AC031977
VERSION	AC031977.7
KEYWORDS	HTG, HTGS, PHASE1, HTGS_DRAFT, HTGS_PULLTOP, HTGS_ACTIVEIN
SOURCE	Human sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS

Unpublished (to 1956)

REFERENCE
2 (1985-1989)
AUTHORS
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Federspiel, N., Glukhov, S., Hansen, Z.S., Hyman, R.,
Morio, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J.,
Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
TITLE
Direct Submission
Submitted (03-APR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304
USA

COMMENT On Mar 4, 2001 this sequence version replaced gi:9665085.

----- Genome Center
Center, Stanford DNA Sequencing and Technology Development

Center
Cancer : Research Data Organization

Center code: SDSTDC
Web site: <http://sequence-www.stanford.edu/group/human/>
Contact: hum-info@sequence.stanford.edu

----- Project Information

Center project name: 880
Center clone name: RP11-288018

Summary Statistics

Sequencing Vector: M13mp18; 100% of reads

Chemistry: Dye-primer; 1% of reads

Chemistry: Dye-terminator Big Dye; 99% of reads

Assembly program: phrap; version 0.950315
Consensus quality: 190680 bases at least Q40

Consensus quality: 191287 bases at least Q30

Consensus quality: 191336 bases at least Q20
Insert size: 195548; agarose-fn

Insert size: 191499; sum-of-contigs

Quality coverage: 7.9x in Q20 bases; agarose-DNA

* NOTE: This is a 'working draft' sequence. It currently has 8.1x in vivo coverage, but only 1.5x in vitro coverage.

* consists of 3 contigs. The true order of the piece

- * is not known and their order in this sequence is arbitrary.
- * Gaps between the contigs are represented by dashes.

* runs of N , but the exact sizes of the gaps are unknown

- * This record will be updated with the finished sequence
- * as soon as it is available and the accession number

* be preserved.

Accession	Contig	Length (bp)
12646	contig of 12646 bp in length	12646
12746	can of unknown length	12746

Accession	Contig	Length
12647	gap of unknown length	12748
12747	contig of 82215 bp in length	94961

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* 94962 95061: gap of unknown length
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Best Local Similarity 99.0%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 4; Indels 16; Gaps 1;

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QY 112 -----CGCTTTTGTCTTCTTCAAGTGAACCTTTTAAATGCAAGACTAAGTGG 164
DB 119197 AACAACACACTTTTGTCTTCTTCAAGTGAACCTTTTAAATGCAAGACTAAGTGG 119256
QY 165 CATTTCAGTACCTTCTTCAATCAATTAAGTCAAAATGCTGGAACATTTGTGACC 224
DB 119257 CATTTCAGTACCTTCTTCAATCAATTAAGTCAAAATGCTGGAACATTTGTGACC 119316
QY 225 TACTCTCATACCCCGTGTACTCAAAATCTCTAAGTGAATTAATGCTTTAAGTAGAAT 284
DB 119317 TACTCTCATACCCCGTGTACTCAAAATCTCTAAGTGAATTAATGCTTTAAGTAGAAT 119376
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DB 120757 AGAGAAATGCTGAGAAATTTTCCACTGAGAGCAAGCAATGTGAATATTTTGGCCAAA 120816
QY 1725 GTTCTTTTATGTCATATGTCATGAGATTTGAAGAGCTATTTTATTTTATATGTTGCA 1784
DB 120817 GTTCTTTTATGTCATATGTCATGAGATTTGAAGAGCTATTTTATTTTATATGTTGCA 120876
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QY 1845 AATCATTTGTTAGCATTTATCCATATATTTTAAATTCAGAAAAATGGTTATCTT 1904
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QY 1905 TAGAATTTGTTAGCATTTATCTTATGTAACGACGCTCTCGATATTAAGC 1964
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QY 2025 AGCCAAAA 2033
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RESULT 8
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LOCUS Human DNA sequence from clone Rpl1-4306 on chromosome 1, complete
DEFINITION
ACCESSION AL583850
VERSION AL583850.5 GI:16973044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Tracey, A.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clones@wellcome.ac.uk
humquey@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:15020514.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
Rpl1-4306 is from the library RPl1-11.2 constructed by the group
of Plesier de Jong. For further details see
http://www.chori.org/bacpac/home.htm

FEATURES
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QY 112 -----CGCTTTGTTCTTTCAGGTAGACACCTTTTAAATGAGAACTAATGAG 164
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QY 2025 AGCCAAAAA 2033
 Db 155052 AGCCTCA 155044

RESULT 9
 AX393338
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 DEFINITION Sequence 268 from Patent WO0210217.
 ACCESSION AX393338
 VERSION AX393338.1 GI:19701341
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
 Endothelial cell expression patterns
 Patent: WO 0210217-A 268 07-FEB-2002;
 The Johns Hopkins University (US)
 Location/Qualifiers
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ORIGIN

Query Match 89.8%; Score 1878.6; DB 6; Length 1909;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1909; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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 Db 421 AAGCTATTTATTTTCAAGAAATGATTTCAATTTGAATCTGTTCTCTAGCGGC 480

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QY 734 CTTCGTAAGAAATTTTAAAGAGAGCTCAGCTTGTTGAAGTGAATGATCTCTTC 793

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QY	1034	TATCTGGCTCAACTGCTATTAACCTCTCGGCTTAATGTCCTCTTCACTTATTAACA	1093
Db	901	TATCTGGCTCAACTGCTATTAACCTCTCGGCTTAATGTCCTCTTCACTTATTAACA	960
QY	1094	AGCAGGTATCGAACACTGCTTCGACAAAGGCTCTTAATGTTAACATTTAGAGCTACTG	1153
Db	961	AGCAGGTATCGAACACTGCTTCGACAAAGGCTCTTAATGTTAACATTTAGAGCTACTG	1020
QY	1154	TTTGTTTAAACAACCTTTTGCACAAATAGGTTCTGAGCGAAAGAGGCAATGACATTT	1213
Db	1021	TTTGTTTAAACAACCTTTTGCACAAATAGGTTCTGAGCGAAAGAGGCAATGACATTT	1080
QY	1214	TAAAGAAAGGCTTTCCGACATCACTTACACATCCCAAACTAAAAAAGTCAACTCTTCC	1273
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QY	1274	AACCTGAGAAAAGCTCTCTGCTTTGAAATGAGAACTTAAAGCAGAGTCACAGCGCAGG	1333
Db	1141	AACCTGAGAAAAGCTCTCTGCTTTGAAATGAGAACTTAAAGCAGAGTCACAGCGCAGG	1200
QY	1334	CAACAACAAGACACAACAACAACATTTGGAATATATATCTCACTCAGCTTTAATATA	1393
Db	1201	CAACAACAAGACACAACAACAACATTTGGAATATATATCTCACTCAGCTTTAATATA	1266
QY	1394	CATCTT-ATTAATTTTCTAGTAGAGAACTACAAATCAGCCTTCAACATTTATATACA	1452
Db	1261	CATCTTATTTATTTTCTAGTAGAGAACTACAAATCAGCCTTCAACATTTATATACA	1320
QY	1453	GTTTAAATAGCCTCTGGAAGTACTCTGTCTGCACGTGAGATTTTTTTCCGCCCA	1512
Db	1321	GTTTAAATAGCCTCTGGAAGTACTCTGTCTGCACGTGAGATTTTTTTCCGCCCA	1386
QY	1513	CCTTGCCCCCTGTCTCCCTCTCTCTCTCCCTTGCAGAGGAATATTTAACATATT	1572
Db	1381	CCTTGCCCCCTGTCTCCCTCTCTCTCTCTCCCTTGCAGAGGAATATTTAACATATT	1440
QY	1573	GGGTCCAACTTCAATATGTAAATATTAATCATTAAGAATTAACCTGCTTCTAGA	1633
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QY	1633	AAAATGCAAGGCTTAAGCATGACAAACAAGAAATGCTGGAATTTGCCACTGG	1692
Db	1501	AAAATGCAAGGCTTAAGCATGACAAACAAGAAATGCTGGAATTTGCCACTGG	1566
QY	1693	AGACAGCAATCTGAATTAATTTTCCCAAAAGTCTTTTATGTCAATATGTGCAGGA	1753
Db	1561	AGACAGCAATCTGAATTAATTTTCCCAAAAGTCTTTTATGTCAATATGTGCAGGA	1620
QY	1753	TTTGAAGAGCATTTTTTTTAAATGTTGCAACTGACAACTCATCTTGGAAAGACAGC	1812
Db	1621	TTTGAAGAGCATTTTTTTAAATGTTGCAACTGACAACTCATCTTGGAAAGACAGC	1677
QY	1813	CAGGGAATGAATGAAAGTGAAGATTTAATCAATTTGTAAAGCATTTATCCCATAT	1877

Db	1680	CAGAGAGATGAGTGAAGGAGGAAAGCTTTTAAATCATCTTGTGTGAAGATTATCCATAT	1739
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Db	1740	ATTTTAAATTCAGAAAAATTTGTCTTATCTTTTGAATTTTGTATTCATATCTTTATGTA	1799
Qy	1933	CTATGTAGCTCATCTCTCTGGATTTAAATTAAGCACCATAATATGATCTGTAAACCAATCA	1992
Db	1800	CTATGTAGCTCATCTCTCTGGATTTAAATTAAGCACCATAATATGATCTGTAAACCAATCA	1859
Qy	1993	CACATATTATATTAATATATATATCTATATTAACGCCAAAAAATTTTTTTT	2041
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LOCUS			linear
DEFINITION	Sequence 341 from patent US 6607879.		PAT 18-DEC-2003
ACCESSION	AR379796		
VERSION	AR379796.1	GI:40087430	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 6005)		
TITLE	Cocks,B.G., Stuart,S.G. and Selthamer,J.J.		
JOURNAL	Compositions for the detection of blood cell and immunological		
FEATURES	Response gene expression		
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Qy	61	AAGCAGTGTGAATAGCCTTCAAGCATGTGAATTACTTCCATCTTCCCGCC-----	112
Db	3971	AAGCAGTGTGAATAGCCTTCAAGCATGTGAATTACTTCCATCTTCCCGCCNNNNNNN	4030
Qy	113	-----GCCTTTTGGTTCTTTTCAAGGAGACACCTTTTAAATGSCAGAACTAATCTGAG	164
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Qy	165	CATTTCAGTAACTTTGCTTTCAAAATCAATAAAGTCAAAATGTATGAAAATTTTGTGCC	224
Db	4091	CATTTCAGTAACTTTGCTTTCAAAATCAATAAAGTCAAAATGTATGAAAATTTTGTGCC	4156
Qy	225	TACCTCCATACCCCGGTACTCAAAATCTCTACGTATGATTAATAGCTTAAAGTAGAT	284
Db	4151	TACCTCCATACCCCGGTACTCAAAATCTCTACGTATGATTAATAGCTTAAAGTAGAT	4210
Qy	285	TCAGTGCCAGAGAACTTGGTGAATTAATTAATTTAA-TTTTTTTTATTCCTTTACA	343
Db	4211	TCAGTGCCAGAGAACTTGGTGAATTAATTAATTTTAAATTTTTTTTATTCCTTTACA	4270
Qy	344	AAGCCATGATTTTATTTGGTGTGATGTGCTGTACACAAGCATTCATAGATG	403
Db	4271	AAGCCATGATTTTATTTGGTGTGATGTGCTGTACACAAGCATTCATAGATG	4330
Qy	404	AGCTGTATATTTTCCAAAGAGTAAATAGACATGCAAAAGTTTCAATAAAACTGGCC	463
Db	4331	AGCTGTATATTTTCCAAAGAGTAAATAGACATGCAAAAGTTTCAATAAAACTGGCC	4390
Qy	464	ATTAACAATTAATTAATTAACCTAATGAATTCCTCTTAGGTTTTTGCAAACTGCT	523

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Db      4451 ATCCATAACAATTTAGAAATGTTGAAGAAAGCTATATATTTTCAGAGAAATGATTT 4510
Qy      584 CATTAATGAACGTGTTCTCCCTAGACAGCCATTTTCCTTTTCTGGAGATTAGCAAG 643
Db      4511 CATTAATGAACGTGTTCTCCCTAGACAGCCATTTTCCTTTTCTGGAGATTAGCAAG 4570
Qy      644 TTATAGAGAGAAATGATCATGATAAGAAAGAAAGAGAGAGAGAGAGAGAGTTAA 703
Db      4571 TTATAGAGAGAAATGATCATGATAAGAAAGAAAGAGAGAGAGAGAGAGAGTTAA 4630
Qy      704 AGTAAGTGTCTAGACCTATGAAAGTAATCCCTTTGCTAGAAATATTTAAGACGCTG 763
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Qy      764 CTGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 823
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Qy      824 AATGAGCTATGATGTAATAATTTATTTATTCATCTAGAAAGCCTTGAAGAGAGAG 883
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Db      4871 GAAATATGATCTCCAAATCCAAAGATGAAACCCAAAGAGAGAGAGAGAGAGAGAG 4930
Qy      1003 TTTTGGACAT-GAAGTTTGTGCACTTTGTTATGCTGTGCTCACTGCTATTTAAACCTC 1061
Db      4931 TTTTGGACATGAAGTTTGTGCACTTTGTTATGCTGTGCTCACTGCTATTTAAACCTC 4990
Qy      1062 TCTGCTATATGATCTCTCACTTCTATTTAGACAGAGATGAAAGAGAGAGAGAGAG 1121
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Qy      1709 TAAATATTTGCCAAAGTTCTTTTATGTCATATAGTGCAGAGATTGAAGAGCTATT 1768
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Qy      1769 TTTTATATGTTCACTAGCACTGATCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1828
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Db      5771 AAGTGAAGGTTTAAATCCATTTGTAACATTTATCCCATATATTTTAAATTCAGAA 5830
Qy      1889 AAATGTTGTTATCTTTAGAAATTTTGTATTCATCTTATATGATCTATGATCTGCT 1948
Db      5831 AAATGTTGTTATCTTTAGAAATTTTGTATTCATCTTATATGATCTATGATCTGCT 5890
Qy      1949 TCTGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2008
Db      5891 TCTGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5950
Qy      2009 TATATATCTATATTAACAGCCAAATTTTAAAGAGAGAGAGAGAGAGAGAGAGAG 2052
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RESULT 11

AK026775

LOCUS Homo sapiens cDNA: FLJ23122 fls, clone UNG08008. 1863 bp mRNA linear PRI 12-SEP-2003

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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TITLE

JOURNAL

REFERENCE

AUTHORS

FEATURES

source

location/qualifiers

/organism="Homo sapiens"

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Query Match      88.3%; Score 1845.6; DB 9; Length 1863;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1859; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 121 GAACCTGGTGAATAAATTTATTTATTTTATTCCTTTACAAAGCATGATTTT 180
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RESULT 12
BC029357 1490 bp mRNA linear PRI 19-NOV-2003
LOCUS BC029357
DEFINITION Homo sapiens cDNA clone MGC:32530 IMAGE:433776, complete cds.
ACCESSION BC029357

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VERSION	BC029357.1	GI:20810417
KEYWORDS	MGC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 1490)	
AUTHORS	Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D., Altschul S.F., Zeeberg B., Bheton K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko T., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stieglitz M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheer T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Grancini P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Boeck S.A., McEwen P.J., McKernan K.U., Malek U.A., Gunaratne P.H., Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W., Villalón D.K., Muzny D.M., Sodergren E.C., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J. and Marz M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE	22388257	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 1490)	
AUTHORS	Strausberg R.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcgdpaxll.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
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Db 1278 GGGTTATAGTCTCTTCATCTTATTAAGACAGCAGTATCGAACCTTGCTTGGACAGG 1337
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RESULT 13
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LOCUS Homo sapiens mRNA; CDNA DKFZps8611524 (from clone DKFZps8611524).
DEFINITION AL157502
ACCESSION AL157502.1 GI:7018552
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1121)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (15-FEB-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZps8611524) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://www.mips.biochem.mpg.de/proj/CDNA/>.
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ORIGIN
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Best Local Similarity 99.6%; Pred. No. 1.1e-202;
Matches 1115; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 936 GAGATAGAAATGTATCTCCACATCCAGCATCGAAGCCAGGGGTAGCAATTCT 995
Db 1 GAGAAATAGAAATGTATCTCCACATCCAGCATCGAAGCCAGGGGTAGCAATTCT 60

QY 996 ATGTAGTTTGGACATGAGTTGGTGCATCTTGTTATGCTGGCTCACTGCTATTA 1055
Db 61 ATGTAGTTTGGACATGAGTTGGTGCATCTTGTTATGCTGGCTCACTGCTATTA 120

QY 1056 AACCTCTGGCTTATAGTCTTCTTCACTTATTAAGACAGCAGTATCGAAGCACTTGGCT 1115
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QY 1116 CGACAAAGGCTCTTAGTAAACATTTAGCAGCTACTGTTGTGTTAAACACACTTTTCA 1175
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QY 1176 CCAATATAGGTTCTGAGGCAACGAGACATGACTATTAAAGAAAGGCTTTCCAGCAT 1235
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QY 1236 CACTTACATCCCAAACTTAAAGATCACTCTTCCACTGAGAAAAGACTCTGAGT 1295
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QY 1296 TTGAATGAAACTTACAGAGAGTCAAGGCCAGGCAACAGCAACACAAACAA 1355
Db 361 TTGAATGAAACTTACAGAGAGTCAAGGCCAGGCAACAGCAACACAAACAA 420

QY 1356 CATTGGATATTTATCTCACTCAAGTTTAAATAATCATCTTATTTTCTAGTAG 1415
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QY 1776 ATGTGCAATACCAACTCATCTTCCGAGACACACCCGAGAAAGAGTAGAGTAA 1835
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QY 1836 AGTTTATTAATCATTTGTGAACATTTATCCCATATTTTAAATTCAGAAAAATTTGT 1895
Db 901 AGTTTATTAATCATTTGTGAACATTTATCCCATATTTTAAATTCAGAAAAATTTGT 960

QY 1896 GTTATATTTAGAAATTTGTATTCATCTTATGATATGATGATGATGATGATGAT 1955
Db 961 GTTATATTTAGAAATTTGTATTCATCTTATGATATGATGATGATGATGATGAT 1020

QY 1956 AATTAAGACCAAAATGATCTGTACACACATATCATATTTATTTAAATATATAT 2015
Db 1021 AATTAAGACCAAAATGATCTGTACACACATATCATATTTATTTAAATATATAT 1080

QY 2016 CTATATTAAGCCCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2055
Db 1081 CTATATTAAGCCCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120

RESULT 14
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LOCUS AX330124
DEFINITION Sequence 633 from Patent WO0194629.
ACCESSION AX330124
VERSION AX330124.1 GI:18103102
KEYWORDS

Thu May 6 14:19:47 2004

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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppe, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
TITLE	Patent: WO 0194629-A 633 13-DEC-2001;
JOURNAL	Avalon Pharmaceuticals (US) Location/Qualifiers
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OY	1758 AGGAGCTATTTTTTTTATGTGTGCACATGCAACTCATCTTCGGAAGACACACCAGA 1817
Db	271 AGGAGCTATTTTTTTTATGTGTGCACATGCAACTCATCTTCGGAAGACACACCAGA 212
OY	1818 GAATGAGTAGAAGTGAAGAGTTTAAATTCATTGTGAACATTATCCCATATATTTT 1877
Db	211 GAATGAGTAGAAGTGAAGAGTTTAAATTCATTGTGAACATTATCCCATATATTTT 152
OY	1878 AATTTCAAAGAAAAATGTGTATCTTTAGAAATTTTGATTCATCAATCTTATGTACTATG 1937
Db	151 AAATTTCAAAGAAAAATGTGTATCTTTAGAAATTTTGATTCATCAATCTTATGTACTATG 92
OY	1938 TGACTCATGCTTCTGGATTAATTAAGCACCAATATGTATCTGTACCAATCACAT 1997
Db	91 TGACTCATGCTTCTGGATTAATTAAGCACCAATATGTATCTGTACCAATCACAT 32
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ACCESSION	AX334654
VERSION	AX334654.1 GI:18125373
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ORGANISM	Homo sapiens
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppe, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
TITLE	Patent: WO 0194629-A 5163 13-DEC-2001;
JOURNAL	Avalon Pharmaceuticals (US) Location/Qualifiers
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ORIGIN	Query Match 15.8%; Score 331; DB 6; Length 331;